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met ser lys asn thr

val ser ser ala arg phe arg lys val asp val asp
glu tyr asp glu asn lys phe val asp glu glu asp
gly gly asp gly gln ala gly pro asp glu gly glu

val asp ser cys leu arg gln gly asn met thr ala

ala leu gln ala ala leu lys asn pro pro ile asn

thr arg ser gln ala val lys asp arg ala gly ser

ile val leu lys val leu ile ser phe lys ala gly

asp ile glu lys ala val gln ser leu asp arg asn

gly val asp leu leu met lys tyr ile tyr lys gly

phe glu ser pro ser asp asn ser ser ala val leu

leu gln trp his glu lys ala leu ala ala gly gly

val gly ser ile val arg val leu thr ala arg lys

FIG. 1

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ggtctgtgtg tgcgt ttctctctct ttttt cgctgcgccc cccgg ggggaggggg gcgcc gaggc atg gcg gg Met Ala G	ttttt tttgcaa gggggg ggaggcg cgcgct gggaggg gg ccc ccg gcc	aga aacagcagcg gag gaggcgggca agg cagcgcgcac cta ccc ccg cc Leu Pro Pro Pr	cegeegeege te geggeggagg ga ggtgeageeg gg g gag aeg geg	cgccgagg 120 ggggagcc 180 ccgggcgg 240 gcg gcc 290
gcc acc acg gcc Ala Thr Thr Ala	gcg gcc gcc g Ala Ala Ala A 20	cc tcg tcg tcc la Ser Ser Ser 25	gcc gct tcc c Ala Ala Ser P	ccg cac 338 ro His 30
tac caa gag tgg Tyr Gln Glu Trp 35	att ctg gac a Ile Leu Asp T	cc atc gac tcg hr Ile Asp Ser 40	ctg cgc tcg c Leu Arg Ser A 45	gc aag 386 rg Lys
gcg cgg ccg gac Ala Arg Pro Asp 50	Leu Glu Arg I	tc tgc cgg atg le Cys Arg Met 55	gtg cgg cgg c Val Arg Arg A 60	gg cac 434 rg His
ggc ccg gag ccg Gly Pro Glu Pro 65	gag cgc acg c Glu Arg Thr A 70	gc gcc gag ctc rg Ala Glu Leu	gag aaa ctg a Glu Lys Leu I 75	tc cag 482 le Gln
cag cgc gcc gtg Gln Arg Ala Val 80	ctc cgg gtc a Leu Arg Val S 85	gc tac aag ggg er Tyr Lys Gly 90	agc atc tcg t Ser Ile Ser T	ac cgc 530 'yr Arg 95
aac gcg gcg cgc Asn Ala Ala Arg	gtc cag ccg c Val Gln Pro P 100	cc cgg cgc gga Pro Arg Arg Gly 105	Ala Thr Pro F	ccg gcc 578 Pro Ala .10
ccg ccg cgc gcc Pro Pro Arg Ala 115	ccc cgc ggg g Pro Arg Gly G	gge cee gee gee Gly Pro Ala Ala 120	gcc gcc gcg c Ala Ala Ala E 125	ccg ccg 626 Pro Pro
ccc acg ccc gcc Pro Thr Pro Ala 130	Pro Pro Pro P	ecg ccc gcg ccc Pro Pro Ala Pro	gtc gcc gcc g Val Ala Ala A 140	gcc gcc 674 Ala Ala
gcc ccg gcc cgg Ala Pro Ala Arg 145	gcg ccc cgc g Ala Pro Arg A 150	geg gee gee gee Ala Ala Ala Ala	gcc gct gcc g Ala Ala Ala A 155	gcc aca 722 Ala Thr
gcg ccc ccc tcg Ala Pro Pro Ser 160	ccc ggc ccc g Pro Gly Pro A 165	gcg cag ccg ggc Ala Gln Pro Gly 170	ccc cgc gcg c Pro Arg Ala C	cag cgg 770 Gln Arg 175
gcc gcg ccc ctg Ala Ala Pro Leu	gcc gcg ccg c Ala Ala Pro P 180	ceg eee geg eee Pro Pro Ala Pro 185	Ala Ala Pro E	ecg gcg 818 Pro Ala 190

FIG. 2A-1

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				Ala	ggc										866
-	_	_	Arg		tcg Ser	_	_	-	-	-	_	_	_		914
					cag Gln										962
					gag Glu 245										1010
		-			cgg Arg	_	-		_				-	_	1058
					ctg Leu										1106
					cgg Arg										1154
					ggg										1202
					cgg Arg 325										1250
					gag Glu										1298
					gag Glu										1346
					cac His										1394
					gcc Ala										1442
					cgg Arg 405										1490

FIG. 2A-2

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gtg tt Val Ph															1538
acc ac Thr Th	c ggg r Gly	cct Pro 435	gac Asp	tcc Ser	ccg Pro	tcc Ser	ccg Pro 440	gtg Val	cct Pro	ttg Leu	ccc Pro	ccc Pro 445	ggg Gly	aag Lys	1586
cca gc Pro Al	c ctc a Leu 450	cca Pro	gga Gly	gcc Ala	gat Asp	ggg Gly 455	acc Thr	ccc Pro	ttt Phe	ggc Gly	tgc Cys 460	cct Pro	gcc Ala	G] À āāā	1634
cgc aa Arg Ly 46	s Glu	aag Lys	ccg Pro	gca Ala	gac Asp 470	ccc Pro	gtg Val	gag Glu	tgg Trp	aca Thr 475	gtc Val	atg Met	gac Asp	gtc Val	1682
gtg ga Val Gl 480	g tac u Tyr	ttc Phe	acc Thr	gag Glu 485	gcg Ala	ggc Gly	ttc Phe	cct Pro	gag Glu 490	caa Gln	gcc Ala	acg Thr	gct Ala	ttc Phe 495	1730
cag ga Gln Gl	g cag u Gln	gag Glu	atc Ile 500	gac Asp	ggc Gly	aag Lys	tcc Ser	ctg Leu 505	ctg Leu	ctc Leu	atg Met	cag Gln	cgc Arg 510	acc Thr	1778
gat gt Asp Va															1826
tat ga Tyr Gl	g cac u His 530	cat His	atc Ile	aag Lys	gtg Val	ctg Leu 535	cag Gln	cag Gln	ggt Gly	cac His	ttc Phe 540	gag Glu	gac Asp	gat Asp	1874
gac cc Asp Pr	o Glu					t ga	agcad	caga	g cc	gccg	cgcc	cct	tgtc	ccc	1926
accccc ggagct cttgct acccct agcccc attggg cctata tcttcc gggaat ttgtcg	ggac to gggac to gagg getce of gggac gggac gggac gggac gggac getce a	tgggo tcatt gagco ctcco gggct tatat cacca ggago agcto	caggo cgcta ctcct cggga catat accao ggtgo	eg ag ac co at gt at gt at gg at gg at gg at ca gg at at gg at	ggggt cccc ccccq cccaq tgc cttgt ccttq ctgct	egeggeetetete	g according actording to the control of the control	etaco tgtgt tetgo tetto teeto teteo tatto	ectg gcct gcct aaaa cctc ctcg ccac	atte	ctgg gcac catt aaaa ccaa tttt tgtc ctct	tag ctg ttg agg cca ggc ccc	gggg cccc aaaa ggtg gcgt ggga gttg	cggggc cagcac cagatc aaaaaa tttatt ggcctt gcagct gttctg	1986 2046 2106 2166 2226 2286 2346 2406 2466 2526 2561

FIG. 2A-3

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asp cys arg ser ser ser asn asn arg Xaa pro lys gly gly ala ala arg ala gly gly pro ala arg pro val ser leu arg glu val val arg tyr leu gly gly ser ser gly ala gly gly arg leu thr arg gly arg val gln gly leu leu glu glu glu ala ala arg gly arg leu glu arg thr arg leu gly ala leu ala leu pro arg gly asp arg pro gly arg ala pro pro ala ala ser ala arg ala ala arg asn lys arg ala gly glu glu arg val leu glu lys glu glu glu glu glu glu asp asp glu asp asp asp asp val val ser glu gly ser glu val pro glu ser asp arg pro ala gly ala gln his his gln leu asn gly gly glu arg gly pro gln thr ala lys glu arg ala lys glu trp ser leu cys gly pro his pro gly gln glu glu gly arg gly pro ala ala gly ser gly thr arg gln val phe ser met ala ala leu ser lys glu gly gly ser ala ser ser thr thr gly pro asp ser pro ser pro val pro leu pro pro gly lys pro ala leu pro gly ala asp gly thr pro phe gly cys pro ala gly arg lys glu lys pro ala asp pro val glu trp thr val met asp val val glu tyr phe thr glu ala gly phe pro glu gln ala thr ala phe gln glu gln glu ile asp gly lys ser leu leu leu met gln arg thr asp val leu thr gly leu ser ile arg leu gly pro ala leu lys ile tyr glu his his ile lys val leu gln gln gly his phe glu asp asp pro glu gly phe leu gly

FIG. 2B

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ala ser ala arg ala ala arg asn lys arg ala qly qlu qlu arg val leu glu lys glu glu glu glu glu glu glu asp asp glu asp asp asp asp val val ser glu gly ser glu val pro glu ser asp arg pro ala gly ala gln his his gln leu asn gly gly glu arg gly pro gln thr ala lys glu arg ala lys glu trp ser leu cys gly pro his pro gly gln glu glu gly arg gly pro ala ala gly ser gly thr arg gln val phe ser met ala ala leu ser lys glu gly gly ser ala ser ser thr thr gly pro asp ser pro ser pro val pro leu pro pro gly lys pro ala leu pro gly ala asp gly thr pro phe gly cys pro ala gly arg lys glu lys pro ala asp pro val glu trp thr val met asp val val glu tyr phe thr glu ala gly phe pro glu gln ala thr ala phe gln glu qln qlu ile asp gly lys ser leu leu leu met gln arg thr asp val leu thr gly leu ser ile arg leu gly pro ala leu lys ile tyr glu his his ile lys val leu gln gln gly his phe glu asp asp pro glu gly phe leu gly FIG 3

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thr arg leu gly ala leu ala leu pro arg gly asp arg pro gly arg ala pro pro ala ala ser ala arg ala ala arg asn lys arg ala gly glu glu arg val leu glu lys glu glu glu glu glu glu asp asp glu asp asp asp asp val val ser glu gly ser glu val pro glu ser asp arg pro ala gly ala gln his his gln leu asn gly gly glu arg gly pro gln thr ala lys glu arg ala lys glu trp ser leu cys gly pro his pro gly gln glu glu gly arg gly pro ala ala gly ser gly thr arg gln val phe ser met ala ala leu ser lys glu gly gly ser ala ser ser thr thr gly pro asp ser pro ser pro val pro leu pro pro gly lys pro ala leu pro gly ala asp gly thr pro phe gly cys pro ala gly arg lys glu lys pro ala asp pro val glu trp thr val met asp val val glu tyr phe thr glu ala gly phe pro glu gln ala thr ala phe gln glu gln glu ile asp gly lys ser leu leu leu met gln arg thr asp val leu thr gly leu ser ile arg leu gly pro ala leu lys ile tyr glu his his ile lys val leu gln gln gly his phe glu asp asp pro glu gly phe leu gly FIG 4

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met lys asn gln asp lys lys asn gly ala ala lys gln pro asn pro lys ser ser pro gly gln pro glu ala gly ala glu gly ala gln gly arg pro gly arg pro ala pro ala arg glu ala glu gly ala ser ser gln ala pro gly arg pro glu gly ala gln ala lys thr ala gln pro gly ala leu cys asp val ser glu glu leu ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn asn gln gly ala pro gly glu asp gly val gln gly glu pro pro glu pro glu asp ala glu lys ser arg ala tyr val ala arg asn gly glu pro glu pro gly thr pro val val asn gly glu lys glu thr ser lys ala glu pro gly thr glu glu ile arg thr ser asp glu val gly asp arg asp his arg arg pro gln glu lys lys lys ala lys gly leu gly lys glu ile thr leu leu met gln thr leu asn thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys tyr ala qlu leu leu glu glu his arg asn ser gln lys qln met lys leu leu gln lys lys gln ser gln leu val qln qlu lys asp his leu arg gly glu his ser lys ala ile leu ala arg ser lys leu glu ser leu cys arg glu leu gln arg his asn arg ser leu lys glu glu gly val gln arg ala arg glu glu glu glu lys arg lys glu val thr ser his phe gln met thr leu asn asp ile gln leu gln met glu gln his asn glu arg asn ser lys leu arg gln glu asn met glu

FIG. 5A

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leu ala glu arg leu lys lys leu ile glu gln tyr glu leu arg glu glu his ile asp lys val phe lys his lys asp leu gln gln leu val asp ala lys leu gln gln ala gln glu met leu lys glu ala glu glu arg his gln arg glu lys asp phe leu leu lys qlu ala val qlu ser gln arg met cys glu leu met lys gln gln glu thr his leu lys gln gln leu ala leu tyr thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser glu val phe thr thr phe lys qln qlu met glu lys met thr lys lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg trp qlu ser ser asn lys ala leu leu glu met ala glu glu lys thr leu arg asp lys glu leu glu gly leu qln val lys ile gln arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp leu asn lys arg val gln asp leu ser ala gly gly gln gly pro val ser asp ser gly pro glu arg arg pro glu pro ala thr thr ser lys glu gln gly val glu gly pro gly ala gln val pro asn ser pro arg ala thr asp ala ser cys cys ala gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu pro thr thr ala thr ala

FIG. 5B

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met ser lys asn thr val ser ser ala arg phe arg lys val asp val asp glu tyr asp glu asn lys phe val asp glu glu asp gly gly asp gly gln ala gly pro asp glu gly glu val asp ser cys leu arg gln gly asn met thr ala ala leu gln ala ala leu lys asn pro pro ile asn thr lys ser gln ala val lys asp arg ala gly ser ile val leu lys val leu ile ser phe lys ala asn asp ile glu lys ala val gln ser leu asp lys asn gly val asp leu leu met lys tyr ile tyr lys gly phe glu ser pro ser asp asn ser ser ala met leu leu gln trp his glu lys ala leu ala ala gly gly val gly ser ile val arg val leu thr ala arg lys thr val

FIG. 6

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A1	103	へしろに	•

															gcc Ala	48
														Tyr	caa Gln	96
															cgg Arg	144
ccg Pro	gac Asp 50	ctg Leu	gag Glu	cgc Arg	atc Ile	tgc Cys 55	cgg Arg	atg Met	gtg Val	cgg Arg	cgg Arg 60	cgg Arg	cac His	ggc Gly	ccg Pro	192
gag Glu 65	ccg Pro	gag Glu	cgc Arg	acg Thr	cgc Arg 70	gcc Ala	gag Glu	ctc Leu	gag Glu	aaa Lys 75	ctg Leu	atc Ile	cag Gln	cag Gln	cgc Arg 80	240
gcc Ala	gtg Val	ctc Leu	cgg Arg	gtc Val 85	agc Ser	tac Tyr	aag Lys	ggg Gly	agc Ser 90	atc Ile	tcg Ser	tac Tyr	cgc Arg	aac Asn 95	gcg Ala	288
				ccg Pro												336
				ggg Gly												384
				ccg Pro												432
				ccc Pro												480
				gcg Ala 165												528
				ccg Pro												576
				cgc Arg												624
Pro				ccg Pro									Gln	Gln		672

FIG. 7A-1

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		cag Gln 230							720
		gcg Ala							768
		ggc Gly							816
		gag Glu							864
		gcg Ala							912
		gcc Ala 310							960
		ctt Leu							1008
		gat Asp							1056
		ggt Gly							1104
		aag Lys							1152
		gat Asp 390							1200
		tcc Ser							1248
		ggg Gly							1296
		cta Leu				Phe	Gly	Cys	1344 7 <b>A-2</b>

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				gag Glu							1392
				tat Tyr 470							1440
				cag Gln							1488
				ctc Leu							1536
				cac His							1584
-	_	-	_	gat Asp			FI	G.	7 <i>F</i>	۷-3	1614

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glu glu arg val leu glu lys glu glu glu glu asp asp asp glu asp glu asp glu asp asp val ser glu gly ser glu val pro glu ser asp arg pro ala gly ala gln his his gln leu asn gly glu arg gly pro gln ser ala lys glu arg val lys glu trp thr pro cys gly pro his gln gly gln asp glu gly arg gly pro ala pro gly ser gly thr arg gln val phe ser met ala ala met asn lys glu gly gly thr ala ser val ala thr gly pro asp ser pro ser pro val pro leu pro pro gly lys pro ala leu pro gly ala asp gly thr pro phe gly cys pro pro gly arg lys glu lys pro ser asp pro val glu trp thr val met asp val val glu tyr phe thr glu ala gly phe pro glu gln ala thr ala phe gln glu gln glu ile asp gly lys ser leu leu leu met gln arg thr asp val leu thr gly leu ser ile arg leu gly pro ala leu lys ile tyr glu his his ile lys val leu qln qln gly his phe glu asp asp pro asp gly phe leu gly

FIG. 7B

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AND THER DOOL FROM ATTERDOOL FROM ATTERDOOL FROM ATTERDOOL FROM ATTERDOOL FROM ATTERDOOL FROM ATTERDO

**ATHEROSCLEROSIS** 

atg Met 1	aag Lys	aac Asn	caa Gln	gac Asp 5	aaa Lys	aag Lys	aac Asn	ggg	gct Ala 10	Ala	aaa Lys	caa Gln	tco Ser	aat Asn 15	cca Pro	48
aaa Lys	ago Ser	agc Ser	cca Pro 20	Gly	caa Gln	ccg Pro	gaa Glu	gca Ala 25	Gly	ccc Pro	gag Glu	gga Gly	gcc Ala 30	Gln	gag Glu	96
cgg Arg	ccc Pro	agc Ser 35	Gln	gcg Ala	gct Ala	cct Pro	gca Ala 40	gta Val	gaa Glu	gca Ala	gaa Glu	ggt Gly 45	ccc Pro	ggc	agc Ser	144
agc Ser	cag Gln 50	gct Ala	cct Pro	cgg Arg	aag Lys	ccg Pro 55	gag Glu	ggt Gly	gct Ala	caa Gln	gcc Ala 60	aga Arg	acg Thr	gct Ala	cag Gln	192
tct Ser 65	ggg Gly	gcc Ala	ctt Leu	cgt Arg	gat Asp 70	gtc Val	tct Ser	gag Glu	gag Glu	ctg Leu 75	agc Ser	cgc Arg	caa Gln	ctg Leu	gaa Glu 80	240
gac Asp	ata Ile	ctg Leu	agc Ser	aca Thr 85	tac Tyr	tgt Cys	gtg Val	gac Asp	aat Asn 90	aac Asn	cag Gln	ggg Gly	ggc Gly	ccc Pro 95	ggc Gly	288
gag Glu	gat Asp	ggg Gly	gca Ala 100	cag Gln	ggt Gly	gag Glu	ccg Pro	gct Ala 105	gaa Glu	ccc Pro	gaa Glu	gat Asp	gca Ala 110	gag Glu	aag Lys	336
tcc Ser	cgg Arg	acc Thr 115	tat Tyr	gtg Val	gca Ala	agg Arg	aat Asn 120	ggg Gly	gag Glu	cct Pro	gaa Glu	cca Pro 125	act Thr	cca Pro	gta Val	384
gtc Val	aat Asn 130	gga Gly	gag Glu	aag Lys	gaa Glu	ccc Pro 135	tcc Ser	aag Lys	ggg Gly	gat Asp	cca Pro 140	aac Asn	aca Thr	gaa Glu	gag Glu	432
atc Ile 145	cgg Arg	cag Gln	agt Ser	gac Asp	gag Glu 150	gtc Val	gga Gly	gac Asp	cga Arg	gac Asp 155	cat His	cga Arg	agg Arg	cca Pro	cag Gln 160	480
gag Glu	aag Lys	aaa Lys	aaa Lys	gcc Ala 165	aag Lys	ggt Gly	ttg Leu	ggt Gly	aag Lys 170	gag Glu	atc Ile	acg Thr	ttg Leu	ctg Leu 175	atg Met	528
cag Gln	aca Thr	Leu	aat Asn 180	act Thr	ctg Leu	agt Ser	Thr	cca Pro 185	gag Glu	gag Glu	aag Lys	ctg Leu	gct Ala 190	gct Ala	ctg Leu	576
tgc Cys	aag Lys	aag Lys 195	tat Tyr	gct Ala	gaa Glu	Leu	ctg Leu 200	gag Glu	gag Glu	cac His	cgg Arg	aat Asn 205	tca Ser	cag Gln	aag Lys	624

FIG. 8A-1

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cag Gln	atg Met 210	Lys	ctc Leu	cta Leu	cag Gln	aaa Lys 215	aag Lys	cag Gln	agc Ser	cag Gln	ctg Leu 220	Val	caa Gln	gag Glu	aag Lys	672
gac Asp 225	His	ctg Leu	cgc Arg	ggt Gly	gag Glu 230	cac His	agc Ser	aag Lys	gcc Ala	gtc Val 235	Leu	gcc Ala	cgc Arg	agc Ser	aag Lys 240	720
ctt Leu	gag Glu	agc Ser	cta Leu	tgc Cys 245	cgt Arg	gag Glu	ctg Leu	cag Gln	cgg Arg 250	cac His	aac Asn	cgc Arg	tcc Ser	ctc Leu 255	aag Lys	768
gaa Glu	gaa Glu	ggt Gly	gtg Val 260	cag Gln	cgg Arg	gcc Ala	cgg Arg	gag Glu 265	gag Glu	gag Glu	gag Glu	aag Lys	cgc Arg 270	aag Lys	gag Glu	. 816
gtg Val	acc Thr	tcg Ser 275	cac His	ttc Phe	cag Gln	gtg Val	aca Thr 280	ctg Leu	aat Asn	gac Asp	att Ile	cag Gln 285	ctg Leu	cag Gln	atg Met	864
gaa Glu	cag Gln 290	cac His	aat Asn	gag Glu	cgc Arg	aac Asn 295	tcc Ser	aag Lys	ctg Leu	cgc Arg	caa Gln 300	gag Glu	aac Asn	atg Met	gag Glu	912
ctg Leu 305	gct Ala	gag Glu	agg Arg	ctc Leu	aag Lys 310	aag Lys	ctg Leu	att Ile	gag Glu	cag Gln 315	tat Tyr	gag Glu	ctg Leu	cgc Arg	gag Glu 320	960
gag Glu	cat His	atc Ile	gac Asp	aaa Lys 325	gtc Val	ttc Phe	aaa Lys	cac His	aag Lys 330	gac Asp	cta Leu	caa Gln	cag Gln	cag Gln 335	ctg Leu	1008
gtg Val	gat Asp	gcc Ala	aag Lys 340	ctc Leu	cag Gln	cag Gln	gcc Ala	cag Gln 345	gag Glu	atg Met	cta Leu	aag Lys	gag Glu 350	gca Ala	gaa Glu	1056
gag Glu	cgg Arg	cac His 355	cag Gln	cgg Arg	gag Glu	aag Lys	gat Asp 360	ttt Phe	ctc Leu	ctg Leu	aaa Lys	gag Glu 365	gca Ala	gta Val	gag Glu	1104
tcc Ser	cag Gln 370	agg Arg	atg Met	tgt Cys	gag Glu	ctg Leu 375	atg Met	aag Lys	cag Gln	caa Gln	gag Glu 380	acc Thr	cac His	ctg Leu	aag Lys	1152
caa Gln 385	cag Gln	ctt Leu	gcc Ala	cta Leu	tac Tyr 390	aca Thr	gag Glu	aag Lys	ttt Phe	gag Glu 395	gag Glu	ttc Phe	cag Gln	aac Asn	aca Thr 400	1200
			agc Ser													1248

FIG. 8A-2

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aag Lys	atg Met	act Thr	aag Lys 420	aag Lys	atc Ile	aag Lys	aag Lys	ctg Leu 425	gag Glu	aaa Lys	gaa Glu	acc Thr	acc Thr 430	atg Met	tac Tyr	1296
			tgg Trp													1344
gag Glu	aaa Lys 450	aca Thr	gtc Val	cgg Arg	gat Asp	aaa Lys 455	gaa Glu	ctg Leu	gag Glu	ggc Gly	ctg Leu 460	cag Gln	gta Val	aaa Lys	atc Ile	1392
			gag Glu													1440
ctg Leu	aac Asn	aag Lys	agg Arg	gta Val 485	cag Gln	gac Asp	ctg Leu	agt Ser	gct Ala 490	ggt Gly	ggc Gly	cag Gln	ggc Gly	tcc Ser 495	ctc Leu	1488
act Thr	gac Asp	agt Ser	ggc Gly 500	cct Pro	gag Glu	agg Arg	agg Arg	cca Pro 505	gag Glu	ggg Gly	cct Pro	ggg Gly	gct Ala 510	caa Gln	gca Ala	1536
ccc Pro	agc Ser	tcc Ser 515	ccc Pro	agg Arg	gtc Val	aca Thr	gaa Glu 520	gcg Ala	cct Pro	tgc Cys	tac Tyr	cca Pro 525	gga Gly	gca Ala	ccg Pro	1584
agc Ser	aca Thr 530	gaa Glu	gca Ala	tca Ser	ggc Gly	cag Gln 535	act Thr	ggg Gly	cct Pro	caa Gln	gag Glu 540	ccc Pro	acc Thr	tcc Ser	gcc Ala	1632
agg Arg 545	_								EI	G.	Q	Λ	2			1638
										U.	$\mathbf{O}$	ヿ゠゙	J			

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

**ATHEROSCLEROSIS** 

lys ser ser pro gly gln pro glu ala gly pro glu gly ala gln glu arg pro ser gln ala ala pro ala val glu ala glu gly pro gly ser ser gln ala pro arg lys pro glu gly ala gln ala arg thr ala gln ser gly ala leu arg asp val ser glu glu leu ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn asn gln gly gly pro gly glu asp gly ala gln gly glu pro ala glu pro glu asp ala glu lys ser arg thr tyr val ala arg asn gly glu pro glu pro thr pro val val tyr gly glu lys glu pro ser lys gly asp pro asn thr glu glu ile arg gln ser asp glu val gly asp arg asp his arg arg pro gln glu lys lys ala lys gly leu gly lys glu ile thr leu leu met gln thr leu asn thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys tyr ala glu leu leu glu glu his arg asn ser gln lys gln met lys leu leu gln lys lys gln ser gln leu val gln glu lys asp his leu arg gly glu his ser lys ala val leu ala arg ser lys leu glu ser leu cys arg glu leu gln arg his asn arg ser leu lys glu glu gly val gln arg ala arg glu glu glu glu lys arg lys glu val thr ser his phe gln val thr leu asn asp ile gln leu gln met glu gln his asn glu arg asn ser lys leu arg gln glu asn met glu leu ala glu arg leu lys lys leu ile glu gln tyr glu leu arg glu glu his ile asp lys val phe lys his lys asp leu gln gln gln leu val asp ala lys leu gln gln ala gln glu met leu lys glu ala glu glu arg his gln arg glu lys asp phe leu leu lys glu ala val glu ser gln arg met cys glu leu met lys gln gln glu thr his leu lys gln gln leu ala leu tyr thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

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AND THEIR USE IN DIAGNOSING AND TREATING

**ATHEROSCLEROSIS** 

glu val phe thr thr phe lys gln glu met glu lys met thr lys lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg trp glu ser ser asn lys ala leu leu glu met ala glu glu lys thr val arg asp lys glu leu glu gly leu gln val lys ile gln arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp leu asn lys arg val gln asp leu ser ala gly gly gln gly ser leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala gln ala pro ser thr glu ala ser gly gln thr gly pro gln glu pro gly ala pro thr ser ala arg ala \*\*\*

FIG. 8B-2

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glu tyr asp glu asn lys phe val asp glu glu asp gly gly asp gly

FIG. 9

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**ATHEROSCLEROSIS** 

1 37		CCT				ATG	TCG		AAC	ACG
73		TCG ser								
109		TAC tyr								
145		GGC gly								
181		GAC asp								
217		CTG leu								
253		AGG <b>arg</b>								
289		GTG val								
325		ATA ile								
361		GTG val								
397										CTC leu
433										GGA gly
469		GGC gly								AAA lys
505	ACC thr		TAG	CCT	AGG		TGC	CTG	CCG	GGG

FIG. 10A

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ATHEROSCLEROSIS

```
AGC GGG AGC TGC CGG TAC AAA GAC CAA AAC GCC CAG
 577
      ATG CCG CCG CTG CCC TGT GGG CGG CGT CTG TTC CCA
 613
      GCT TCG CTT TTT CCC TTT CCC GTG TCT GTC AGG ATT
      ACA TAA GGT TTC CCT TCG TGA GAA TCG GAG TGG CGC
 649
      AGA GGG TCC TGT TCA TAC GCG CCG TGC GTC CGG CTG
 685
 721
      TGT AAG ACC CCT GCC TTC AGT GTC CTT GAG CAA CGG
 757
      TAG CGT GTC GCC GGC TGG GTT TGG TTT TGT CGT GGA
      GGG ATC TGG TCA GAA TTT GAG GCC AGT TTC CTA ACT
 793
      CAT TGC TGG TCA GGA AAT GAT CTT CAT TTA AAA AAA
 829
      AAA AAA AGA CTG GCA GCT ATT ATG CAA AAC TGG ACC
 865
 901
      CTC TTC CCT TAT TTA AGC AGA GTG AGT TTC TGG AAC
      CAG TGG TGC CCC CCC CGC CGC CGC CGC CGT CCT
 937
      GCT CAA GGG AAG CCT CCC TGC AGA GCA GCA GAG CCC
 973
      CTG GGC AGG AGC GCC GCG TCC CGC TCC CAG GAG ACA
1009
      GCA TGC GCG GTC ACG CGG CAC TTC CTG TGC CTC CCA
1045
      GCC CCA GTG CCC CGG AGT TCT TCA GGG CGA CAG GGA
1081
      CCT CAG AAG ACT GGA TCC GAT CCA GAC AGA CGC CCA
1117
1153
      TTC TTG GTT CAG CTC AGT GTT TTC AAA AGG AAC GTG
1189
      CTA CCG TGG GTA GAG CAC ACT GGT TCT CAG AAC ACG
      GCC GGC GCT TGA CGG TTG TCA CAG CTC CAG AAC AAA
1225
1261
      TCC TGG GAG ACA GGC GAG CGC GAG TCG CCG GGC AGG
1297
      AAT TCC ACA CAC TCG TGC TGT TTT TGA TAC CTG CTT
1333
      TTT GTT TTG TTT TGT AAA AAT GAT GCA CTT GAG AAA
      ATA AAA CGT CAG TGT TGA CAA AAA AAA AAA AAA AAA
1369
```

FIG. 10B

GAC TGC CGC AGC AGC AGC AAC CGC TAG CCG AAG asp cys arg ser ser ser asn asn arg Xaa pro lys GGT GGC GCG CGG GCC GGC CCG GCG CGC gly gly ala ala arg ala gly gly pro ala arg pro 73 GTG AGC CTG CGG GAA GTC GTG CGC TAC CTC GGG GGT val ser leu arg glu val val arg tyr leu gly gly 109 AGC AGC GGC GGC GGC CGC CTG ACC CGC GGC CGC ser ser gly ala gly gly arg leu thr arg gly arg 145 GTG CAG GGT CTG CTG GAA GAG GAG GCG GCG CGG val gln gly leu leu glu glu glu ala ala arg 181 GGC CGC CTG GAG CGC ACC CGT CTC GGA GCG CTT GCG gly arg leu glu arg thr arg leu gly ala leu ala 217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG leu pro arg gly asp arg pro gly arg ala pro pro 253 GCC GCC AGC GCC GCG GCG CGG AAC AAG AGA GCT ala ala ser ala arg ala ala arg asn lys arg ala 289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG gly glu glu arg val leu glu lys glu glu glu glu GAG GAG GAA GAC GAC GAC GAC GAC GAC 325 glu glu glu asp asp glu asp asp asp asp GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT 361 val val ser glu gly ser glu val pro glu ser asp 397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC arg pro ala gly ala gln his his gln leu asn gly GGC GAG CGC GGC CAG ACC GCC AAG GAG CGG GCC 433 gly glu arg gly pro gln thr ala lys glu arq ala AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG 469

**FIG. 11A** 

lys glu trp ser leu cys gly pro his pro gly gln

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AND THEIR USE IN DIAGNOSING AND TREATING

ATHEROSCLEROSIS

505			A GGG									ACC thr
541			GTG val									
577	gGG gly		TCA									
613			ccg pro									
649	CTC leu		. GGA gly									
685			CGC arg									
721			GTC val									
757	GCG ala		TTC phe									
793			ATC ile									
829	CGC arg		GAT asp									
865	gly		GCG ala									
901	GTG val		CAG gln									
937			TTC phe			TGA	GCA	CAG	AGC	CGC	CGC	GCC
		CTC TGG	CAT ACT	GTC GGG	ACC CAG	CAA GCG	GGT AGG	GTC GGT	CCA GCG	GAG GAC	GCC CTA	AGG CCC

FIG. 11B

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ATHEROSCLEROSIS

```
TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG
1117
      CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC
1153
      TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG
1189
      CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA
1225
      AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC
1261
      TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA
1297
      GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT
1333
      TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC
1369
      TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT
1405
1441
      CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG
1477
      GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC
      GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT
1513
      TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT
1549
      TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA
1585
```

FIG. 11C

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS

AND THEIR USE IN DIAGNOSING AND TREATING

**ATHEROSCLEROSIS** 

256		GCC ala				
289		CGA arg				
325		GAA glu				
361		GAG glu				
397		GGT gly				
433		GGC gly				
469		TCG ser				
505		CGG arg				
541		TTC phe				
577		GCC ala				
613		GTG val				
649		GCC ala				
685		AAA lys				
721		ATG met				

FIG. 12A

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ATHEROSCLEROSIS

757	GCG ala	ggc gly										
793	CAG gln	GAG glu										
829		ACC thr										
865		CCA pro										
901		CTG leu										
937		GGC gly				TGA	GCA	CAG	AGC	CGC	CGC	GCC
973	CCT	TGT	CCC	CAC	CCC	CAC	CCC	GCC	TGG	ACC	CAT	TCC
1009	TGC	CTC	CAT	GTC	ACC	CAA	GGT	GTC	CCA	GAG	GCC	AGG
1045	AGC	TGG	ACT	GGG	CAG	GCG	AGG	GGT	GCG	GAC	CTA	CCC
1081	TGA	TTC	TGG	TAG	GGG	GCG	GGG	CCT	TGC	TGT	GCT	CAT
1117	TGC	TAC	CCC	CCC	ACC	CCG	TGT	GTG	TCT	CTG	CAC	CTG
1153		CCA										
1189		GAC										
1225		CCT										
1261		AAA										
1297		GAA										
1333		GTT				ATA						
1369		GCC										
1405		CCT										
1441 1477		GGG										
1513		GGT										
1513		TAA										
1585		ATA										T T T
1303			* ** ** 7		-1111	1111	1110	JAA	11111	17077	TITI	

FIG. 12B

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING

**ATHEROSCLEROSIS** 

196						GGA gly		
217		CCC pro						
253		GCC ala						
289		GAG glu						
325		GAG glu						
361		GTG val						
397		CCC pro						
433	GGC gly	GAG glu						
469		GAG glu						
505		GAA glu						
541		CAG gln						
577		GGA gly						
613	CCG pro	TCC ser						
649		CCA pro						

FIG. 13A

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685												GAG glu
721												GAG
												glu
757	GCG											
	ala	gly	phe	pro	glu	gln	ala	thr	ala	phe	gln	glu
793	CAG	GAG	ATC	GAC	GGC	AAG	TCC	CTG	CTG	CTC	ATG	CAG
	gln	glu	ile	asp	gly	lys	ser	leu	leu	leu	met	gln
829	CGC	ACC	GAT	GTC	CTC	ACC	GGC	CTG	TCC	ATC	CGC	CTG
	arg	thr	asp	val	leu	thr	gly	leu	ser	ile	arg	leu
865	GGG	CCA	GCG	TTG	AAA	ATC	TAT	GAG	CAC	CAT	ATC	AAG
	gly	pro	ala	leu	lys	ile	tyr	glu	his	his	ile	lys
901	GTG	CTG	CAG	CAG	GGT	CAC	TTC	GAG	GAC	GAT	GAC	CCG
						his						
937	GAA					TGA	GCA	CAG	AGC	CGC	CGC	GCC
	glu	gly	phe	leu	gly							
973	CCT	TGT	CCC	CAC	CCC	CAC	CCC	GCC	TGG	ACC	CAT	TCC
1009	TGC	CTC	CAT	GTC	ACC	CAA	GGT	GTC	CCA	GAG	GCC	AGG
1045						GCG						
1081						GCG						
1117						CCG						
1153						TCC						
1189						CTC						
1225						CTG						
1261						AAA						
1297						AGA						CCA
1333						ATA						TGT
1369						TTT						TTC
1405						ACT						
1441						AGC						
1477						CTG					TCT	CCC
1513						GCT						GCT
1549						GAA						TTT
1585	TAA	ATA	AAA	TTT	TAA	AAA	AAG	GAA	AAA	AAA	AAA	

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AND THEIR USE IN DIAGNOSING AND TREATING **ATHEROSCLEROSIS** 

	GTG CCC								ATG	AAG		CAA
73											AAC asn	
109											GCG <b>ala</b>	
145	GGA gly										CCC pro	
181											CCC pro	
217	AGG <b>arg</b>										CAG gln	
253	GGG gly										AGC ser	
289	CAG gln										GTG val	
325	AAC asn										GTC val	
		glu	pro	pro	glu	pro	glu	asp	ala	glu	lys	ser
397												CCG pro
433												TCC ser
469												AGC ser
505												CAG gln

**ATHEROSCLEROSIS** 

541	GAA glu										GAG glu	
577											AGC ser	
613											AAG lys	
649	GCG ala										CAG gln	
685	CAG gln										CAG gln	
721	GTG val										CAC his	
757											AGC ser	
793											CTC leu	
829	GAA glu										GAG glu	
865	lys	arg	lys	glu	val	thr	ser	his	phe	gln	ATG met	thr
901	CTC leu											AAC asn
937	GAG glu											GAG glu
973	leu	ala	glu	arg	leu	lys	lys	leu	ile	glu	gln	TAC tyr
1009												AAA lys

FIG. 14B

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1045						AAG lys
1081	CAG gln					
1117	CGG arg					
1153	GCC ala					
1189	CAA gln					
1225	TAC tyr					
1261	TCC ser					
1297	GAA glu					
1333	GAG glu					
1369	AGC ser					
1405	AAA lys					CTG leu
1441	GTG val					
1477	CTG leu					
1513	CAG gln					

FIG. 14C

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**ATHEROSCLEROSIS** 

1549												GCC
	ser	asp	ser	gly	pro	glu	arg	arg	pro	glu	pro	ala
1585	ACC	ACC	TCC	AAG	GAG	CAG	GGT	GTC	GAG	GGC	CCC	GGG
						gln						
				•	J		J .		<b>J</b>	J 1	r	J-1
1621	GCT	CAA	GTA	CCC	AAC	TCT	CCA	AGG	GCC	ACA	GAC	GCT
	ala	gln	val	pro	asn	ser	pro	arg	ala	thr	asp	ala
1657	шаа	maa.	maa	G G A	com	CCA	999	7.00	202	<b>~</b> ~ ~	~ <b>~ ~ ~</b>	
102/						GCA						
	SEL	Cys	Cys	ата	ЭтУ	ala	pro	ser	CIII	gru	ата	ser
1693	GGC	CAG	ACA	GGG	CCC	CAG	GAG	CCC	ACC	ACT	GCC	ACT
	gly	gln	thr	gly	pro	gln	glu	pro	thr	thr	ala	thr
1729	GCC	TAG	AGA	GCT	TGG	TGC	TGG	GGT	GTG	CCA	GGA	AGG
	ala											
1765	GAG	CAG	GCA	GCC	CAG	CCA	GGC	CTG	GCC	CAG	CCC	AGG
1801						GTC						
1837	GTT	CTG	ACC	TGG	CTG	GCA	CCT	GAC	CCT	CTG	CAG	TCT
1873						AGT						
1909	ACA	TGC	AAG	GCC	TCA	CAC	ATT	TGT	GTC	TCT	AAG	TGT
1945	ACT	GTG	GGC	TTG	CAT	CGG	GGG	TGA	CGA	TGG	ACA	GAT
1981	GAA	GCC	AGC	GGC	TCC	CTT	GTG	AGC	TGA	AGT	CTT	ACG
2017	GAG	GAG	ACG	GCG	TCT	GCA	CTG	CCA	TCG	CAG	TGA	CCT
2053	GCA	GGA	CGA	GTT	CCT	TGA	GCT	TTC	CCT	GCC	TGC	TTT
2089	GAG	GCT	GAG	ACC	CCT	CCC	GGC	CCT	TCA	GAG	CTC	CTG
2125	ACA	GGT	GAT	ACA	CAC	CCA	GCC	TTG	ACC	GCA	CTT	CTC
2161	TTG	GGT	AGC	TGG	GCT	CTC	CTA	GCC	TCC	CCC	AGA	GGC
2197	GCC	ATT	GCT	TCT	CTT	GAC	TTG	GAG	AGG	GGA	TGC	CCA
2233						GGC						
2269	GGC	TGC	TCT	CCT	GCC	TCG	AGC	AGG	GGC	AGG	AGT	GTT
2305	TCT	GGT	GGG	ATG	ATG	CGC	TCG	CTG	GTC	AGG	AGC	CCC
2341	GTG	GGC	GCT	GCT	TCC	CCC	GCC	CTC	TGG	TGA	TGC	CAG
2377	GAC	CAG	GCC	AGT	GAT	GCT	TCT	CAG	TAG	CCT	TAC	CAT
2413	TCA	CAG	GTG	CCT	CTC	CAG	CCC	GCA	CAG	TGA	GTG	ACA
2449	AGA	TCA	TCC	AAA	GGA	TTC	CTT	CTG	AAG	GTG	TTC	GTT
2485	TCG	TTT	TGT	TTT	GTT	GCA	CGT	GAC	GGT	TTG	TAT	TGA
2521	GGA	CCC	TCT	GAG	GAA	GAG	GGG	TGC	TGT	AGC	AGT	GGT
2557	CCC	TGC	GTG	CCT	GGC	TCC	AGT	GTC	CTG	CCC	TCC	CCC
2593	CCC	TCG	CCA	TGG	CTC	CTC	GGC	CGC	CTT	GGT	GCT	GAG
2629	GTT	TCT	GTT	TGG	TGA	GAT	CAG	GTT	GTC	TGT	TCA	GAG

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ATHEROSCLEROSIS

	2665	AG	A AG	A GGC	GTC	TGA	A TGO	CTI	TGC	CGC	CAG	CTT	' GCC
	2701	TG	C GG(	G CCI	CAA	TCC	CGG	GAG	GCC	GCC	CGG	TTC	CCG
	2737	TC	A CTO	TTC	TCC	CCG	TGC	AGI	GCG	TTG	CTG	GTC	CCC
	2773	AG	G AC	CAGC	TGC	TCG	TTT	GCI	' GTA	TGG	GTC	AGT	TTC
	2809	TG	C TTC	CTG	CCC	CCC	CACT	CCA	CCT	AAC	TGC	AAT	CCT
	2845	TGO	G GG	TTC	CCT	GGI	TCT	CGT	, CCC	TGG	TAC	CTC	TGT
	2881	GC	CAA	A GAA	GTA	GCC	TTC	TTT	' GGG	ATT	CTT	GTT	CTG
	2917	CCC	ATC	G CGG	GAG	CTG	CTG	CTG	TCT	GAC	AGG	TGA	GGC
	2953	CTC	G AGA	A CTC	AGC	GGC	TGA	CAG	AGC	TGC	AGA	GCT	CTG
	2989	CAC	GGI	GGC	TCC	CGG	GGC	GGC	CTC	TGT	GTG	CTG	CAC
	3025	ACC	GCI	GCT	CTG	CTG	GCA	CTG	GCC	AGT	CTG	TGC	AGA
	3061	GCA	LTT	'GAG	TAC	TGG	CTC	AGG	AGG	GAG	GGÇ	TCT	GCT
	3097	GGC	CTC	GAG	GGA	CAG	CGC	CAC	GTC	TCC	AGC	TGG	GCT
;	3133	CAG	GGA	GAG	CCC	CAG	ACT	GGC	TGC	GTA	GGG	TGC	TTG
;	3169	GGG	TTT	' GCT	TCT	TGC	AGT	ATT	TCT	TGG	AAG	CTG	TTT
	3205	TGT	TGT	CCT	GCT	ATT	CCT	TCA	TCT	TCC	ACA	GTC	CAC
3	3241	GCT	CAG	CCT	TTA	ACT	TGG	ATC	CCT	CAC	ATA	ACA	GGG
3	3277	TTC	ATG	AGA	CCC	GCA	AGT	ACG	CCC	AAG	CTA	CGT	ATG
3	3313	GCT	GAG	GCC	AGC	TGG	CAG	GTG	AAT	GGC	ACG	CCA	TTG
3	3349	CTG	CTG	CTA	ATC	CCT	GGC	ATA	TCT	TTA	GTT	CAC	CTC
3	3385	GAA	ATG	CCC	CCG	CCA	CAG	TGC	AAG	CAG	TGA	GTC	CAC
3	3421	GTG	CCA	CCC	TGG	GCT	GAA	TCC	CAC	CCC	CTG	TGA	GTG
3	3457	TTG	CCC	GAG	ATT	GTG	TCT	CTT	CTG	AAT	GCC	TTC	ACT
3	3493	GGG	AAT	GGC	CTC	TGC	CGC	CTC	CTG	CTC	AGG	GAG	GCT
3	3529		CCC		CCT					CAG	ACT	GAG	GTA
3	3565	CAA	GAA	CCG						GTG	TGG	CTA	GGC
3	8601	GCC	AGG		CAG					TAG	CTG	CCT	GCA
3	8637	CCC	TTG						ACG	GTG	GCC	TCC	ATC
3	673	CTG	GCT		CTC			GCT	ACC	TCG	CAT	AGC	CCA
_	709		GTG		CTA				AGG			GGA	TGG
	745			GCA									TTC
	781			CAG									
	817			TCC									
	853			AGA									
	889			ATC									
	925			TTT									
	961			CAT									
	997			GGC									
	033			CCG									
	069			CCA									
	105			CCC									
	141			CAG									
4	177	GTG	TCC	GGA	CCT	TGT	CCA	GCT	GAG	CGC	TTC	GTG	TAT
							_		_				

FIG. 14E

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ATHEROSCLEROSIS

```
4213
      GAC TCA GCT TCG TGT GTG AGT CCA GCG GAG TGC GTC
4249
      ACG TGA CCT AGA CTC AGC GGT GTC AGC CGC ACT TTG
      ATT TGT TTG TTT TCC ATG AGG TTT TTG GAC CAT GGG
4285
      CTT AGC TCA GGC AAC TTT TCT GTA AGG AGA ATG TTA
4321
4357
      ACT TTC TGT AAA GAT GCT TAT TTA ACT AAC GCC TGC
4393
      TTC CCC CAC TCC CAA CCA GGT GGC CAC CGA GAG CTC
4429
      ACC AGG AGG CCA ATA GAG CTG CTC CAG CTC TCC CAT
4465
      CTT GCA CCG CAC AAA GGT GGC CGC CCC AGG GAC AGC
4501
      CAG GCA CCT GCC TGG GGG AGG GGC TTC TCT TCC TTA
4537
      TGG CCT GGC CAT CTA GAT TGT TTA AAG TTG TGC TGA
4573
      CAG CTT TTT TTG GTT TTT TGG TTT TTG TTT
      TTG TTT TTG TTT TTG TCT ACT TTT GGT ATT CAC AAC
4609
     AGC CAG GGA CTT GAT TTT GAT GTA TTT TAA GCC ACA
4645
4681
     TTA AAT AAA GAG TCT GTT GCC TTA AAA AAA AAA AAA
     AAA AAA
4717
```

**FIG. 14F** 

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1 37 73 109	CCG AGA	GGT GGC	TCA AGT AGC GGG	GGG GCC ATG	TTG AAG TCG	CTG AAG AAG	GGC AGG AAC	TGG CCT ACA	GCT TTG GTG	TGC CCG	TGA CTG TCG	GGT GTC GCC
145			CGG arg									
181			TTC phe									
217			GGG gly									
253			CAA gln									
289			AAG lys									
325			AAG lys									
361			ATC ile									
397			CAA gln									
433			AAG lys									
469			AAT asn									
505	glu	lys	ala	leu	ala	ala	gly	gly	val	gly	ser	ile
541			GTC val								TAG	TCT

FIG. 15A

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GGC AGG AAG TGG ATT ATC TGC CTC GGG AGT GGG AAT 577 613 TGC TGG TAC AAA GAC CAA AAC AAC CAA ATG CCA CCG CTG CCC TGT GGG TAG CAT CTG TTT CTC TCA GCT TTG 649 CCT TCT TGC TTT TTC ATA TCT GTA AAG AAA AAA ATT 685 ACA TAT CAG TTG TCC CTT TAA TGA AAA TTG GGA TAA 721 757 TAT AGA AGA AAT TGT GTT AAA ATA GAA GTG TTT CAT CCT TTC AAA ACC ATT TCA GTG ATG TTT ATA CCA ATC 793 TGT ATA TAG TAT AAT TTA CAT TCA AGT TTT AAT TGT 829 GCA ACT TTT AAC CCT GTT GGC TGG TTT TTG GTT CTG 865 TTT GGT TTT GTA TTA TTT TTA ACT AAT ACT GAA AAA 901 TTT GGT CAG AAT TTG AGG CCA GTT TCC TAG CTC ATT 937 GCT AGT CAG GAA ATG ATA TTT ATA AAA AAT ATG AGA 973 GAC TGG CAG CTA TTA ACA TTG CAA AAC TGG ACC ATA 1009 TTT CCC TTA TTT AAT AAG CAA AAT ATG TTT TTG GAA 1045 1081 TAA GTG GTG GGT GAA TAC CAC TGC TAA GTT ATA GCT TTG TTT TTG CTT GCC TCC TCA TTA TCT GTA CTG TGG 1117 GTT TAA GTA TGC TAC TTT CTC TCA GCA TCC AAT AAT 1153 CAT GGC CCC TCA ATT TAT TTG TGG TCA CGC AGG GTT 1189 CAG AGC AAG AAG TCT TGC TTT ATA CAA ATG TAT CCA 1225 TAA AAT ATC AGA GCT TGT TGG GCA TGA ACA TCA AAC 1261 TTT TGT TCC ACT AAT ATG GCT CTG TTT GGA AAA AAC 1297 1333 TGC AAA TCA GAA AGA ATG ATT TGC AGA AAG AAA GAA AAA CTA TGG TGT AAT TTA AAC TCT GGG CAG CCT CTG 1369 AAT GAA ATG CTA CTT TCT TTA GAA ATA TAA TAG CTG 14:05 1441 CCT TAG ACA TTA TGA GGT ATA CAA CTA GTA TTT AAG ATA CCA TTT AAT ATG CCC EGT AAA TGT CTT CAG TGT 1477 TCT TCA GGG TAG TTG GGA TCT CAA AAG ATT TGG TTC 1513 1549 AGA TCC AAA CAA ATA CAC ATT CTG TGT TTT AGC TCA GTG TTT TCT AAA AAA AGA AAC TGC CAC ACA GCA AAA 1585 1621 AAT TGT TTA CTT TGT TGG ACA AAC CAA ATC AGT TCT CAA AAA ATG ACC GGT GCT TAT AAA AAG TTA TAA ATA 1657 TCG AGT AGC TCT AAA ACA AAC CAC CTG ACC AAG AGG 1693 GAA GTG AGC TTG TGC TTA GTA TTT ACA TTG GAT GCC 1729 AGT TTT GTA ATC ACT GAC TTA TGT GCA AAC TGG TGC 1765 AGA AAT TCT ATA AAC TCT TTG CTG TTT TTG ATA CCT 1801 GCT TTT TGT TTC ATT TTG TTT TGT TTT GTA AAA ATG 1837 ATA AAA CTT CAG AAA ATA AAA TGT CAG TGT TGA ATA 1873 ATT AAA AAA AAA AA 1909

GAA GAG CGA GTA CTT GAG AAA GAA GAG GAA GAA GAT glu glu arg val leu glu lys glu glu glu glu asp GAT GAA GAT GAA GAT GAA GAT GAT GTG TCA 37 asp asp glu asp glu asp glu asp asp val ser 73 GAG GGC TCT GAA GTG CCC GAG AGT GAC CGT CCT GCA glu gly ser glu val pro glu ser asp arg pro ala 109 GGT GCC CAG CAC CAG CTT AAC GGC GAG CGG GGA gly ala gln his his gln leu asn gly glu arg gly CCT CAG AGT GCC AAG GAG AGG GTC AAG GAG TGG ACC 145 pro gln ser ala lys glu arg val lys glu trp thr 181 CCC TGC GGA CCG CAC CAG GGC CAG GAT GAA GGG CGG pro cys gly pro his gln gly gln asp glu gly arg GGG CCA GCC CCG GGC AGC GGC ACC CGC CAG GTG TTC 217 gly pro ala pro gly ser gly thr arg gln val phe TCC ATG GCA GCC ATG AAC AAG GAA GGG GGA ACA GCT 253 ser met ala ala met asn lys glu gly gly thr ala TCT GTT GCC ACC GGG CCA GAC TCC CCG TCC CCC GTG 289 ser val ala thr gly pro asp ser pro ser pro val CCT TTG CCC CCA GGC AAA CCA GCC CTA CCT GGG GCC 325 pro leu pro pro gly lys pro ala leu pro gly ala GAC GGG ACC CCC TTT GGC TGT CCT CCC GGG CGC AAA 361 asp gly thr pro phe gly cys pro pro gly arg lys 397 GAG AAG CCA TCT GAT CCC GTC GAG TGG ACC GTG ATG glu lys pro ser asp pro val glu trp thr val met 433 GAT GTC GTC GAA TAT TTT ACT GAG GCT GGA TTC CCG asp val val glu tyr phe thr glu ala gly phe pro 469 GAG CAG GCG ACA GCT TTC CAA GAG CAG GAA ATT GAT qlu gln ala thr ala phe gln glu gln glu ile asp

FIG. 16A

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505		AAA lys										
541		ACC thr										
577	AAA lys	ATC ile										
613		CAC his										
649	GGC gly	TGA	GCG	CCC	AGC	CTC	ACC	CCT	GCC	CCA	GCC	CAT
685	TCC	GGC	CCC	CAT	CTC	ACC	CAA	GAT	CCC	CCA	GAG	TCC
721	AGG	AGC	TGG	ACG	GGG	ACA	CCC	TCA	GCC	CTC	ATA	ACA
757	GAT	TCC	AAG	GAG	AGG	GCA	CCC	TCT	TGT	CCT	TAT	CTT
793	TGC	CCC	TTG	TNT	CTG	TCT	CAC	ACA	CAT	CTG	CTC	CTC
829	AGC	ACG	TCG	GTG	TGG	GGA	GGG	GAT	TGC	TCC	TTA	AAC
865	CCC	AGG	TGG	CTG	ACC	CTC	CCC	ACC	CAG	TCC	AGG	ACA
901	TTT	TAG	GAA	AAA	AAA	AAT	GAA	ATG	TGG	GGG	GCT	TCT
937	CAT	CTC	CCC	AAG	ATC	CTC	TTC	CGT	TCA	GCC	AGA	TGT
973	TTC	CTG	TAT	AAA	TGT	TTG	GAT	CTG	CCT	GTT	TAT	TTT
1009	GGT	GGG	TGG	TCT	TTC	CTC	CCT	CCC	CTA	CCA	CCC	ATG
1045		CCC										
1081		GGA										
1117		TCC							TGA			
1153		CTG						AAT	ATT	GCA	CCG	AAG
1189	GII	TTT	TAM	AIA	AAA	TII	ΙA					

FIG. 16B

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1	CA	AAA	AGC	AGC	CCA	GGA	CAA	CCG	GAA	GCA	GGA	CCC	GAG	GGA	GCC
		lys	ser	ser	pro	gly	gln	pro	glu	ala	gly	pro	glu	gly	ala
45	CAG	GAG	CGG	רכר	AGC	CAG	GCG	GCT	ССТ	GCA	СТД	GDD	GCA	GAA	CCT
			arg												
				•											
90			AGC												
	pro	дтХ	ser	ser	gın	aıa	pro	arg	Tys	pro	giu	gīy	ala	gin	ala
135	AGA	ACG	GCT	CAG	TCT	GGG	GCC	CTT	CGT	GAT	GTC	TCT	GAG	GAG	CTG
	arg	thr	ala	gln	ser	gly	ala	leu	arg	asp	val	ser	glu	glu	leu
100	700	ccc	(1 N N	ama	<i>~</i>	an a	2012	C.T.C	200	202	mr. c	mam	ата	a. a	
180			CAA gln												
	301	urg	9111	ieu	gru	asp	116	reu	261	CIII	CYL	cys	vai	asp	asıı
225			GGG												
	asn	gln	gly	gly	pro	gly	glu	asp	gly	ala	gln	gly	glu	pro	ala
270	GAA	CCC	GAA	САТ	GCA	GAG	AAG	<b>ጥ</b> ሮር	CGG	ACC	тдт	GTG.	GCA	ACC	ידי א
270			glu												
315			CCT												
	gly	glu	pro	glu	pro	thr	pro	val	val	tyr	gly	glu	lys	glu	pro
360	TCC	AAG	GGG	GAT	CCA	AAC	ACA	GAA	GAG	ATC	CGG	CAG	AGT	GAC	GAG
			gly												
		~~~	<b>~~</b>	~~~	~~~										
405			GAC												
	val	9-1	asp	arg	asp	IIIS	arg	ary	pro	gin	giu	TAR	rys	rys	ara
450	AAG	GGT	TTG	GGG	AAG	GAG	ATC	ACG	TTG	CTG	ATG	CAG	ACA	TTG	AAT
	lys	gly	leu	gly	lys	glu	ile	thr	leu	leu	met	gln	thr	leu	asn
495	א כיידי	כידיכ	AGT	אככ	CCA	GNG	G N G	אאכ	CTC	CCT	CCT	CTC	TCC	7 7 C	7 7 C
473			ser												
					•	<b>J</b>	<b>J</b>						- 2 -	-1-	-7-
540			GAA												
	tyr	ala	glu	leu	leu	glu	glu	his	arg	asn	ser	gln	lys	gln	met
585	AAG	CTC	CTA	CAG	AAA	AAG	CAG	AGC	CAG	CTG	GTG	CAA	GAG	AAG	GAC
			leu												
														_	
630			CGC												
	his	Ieu	arg	дтХ	glu	nis	ser	Tys	ala	val	leu	ala	arg	ser	1ys
675	CTT	GAG	AGC	CTA	TGC	CGT	GAG	CTG	CAG	CGG	CAC	AAC	CGC	TCC	CTC
- · <del>-</del>			ser												
										-			_		

FIG. 17A

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720															CGC arg
765															CAG gln
810															CAA gln
855															CAG gln
900						GAG glu									AAG lys
945						CTG leu									
990						GCA ala									
1035						GCA ala									
1080						ACC thr									
1125						GAG glu									
1170	GAG glu					TTC phe									
1215	AAG lys					GAG glu									
1260	TGG trp	glu	ser	ser	asn	lys	ala	leu	leu	glu	met	ala	glu	glu	lys
1305	ACA thr														
1350	CGG arg	leu	glu	lys	leu	cys	arg	ala	leu	gln	thr	glu	arg	asn	asp
1395	CTG .														
1440	CTC :														

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CAA GCA CCC AGC TCC CCC AGG GTC ACA GAA GCG CCT TGC TAC CCA gln ala pro ser ser pro arg val thr glu ala pro cys tyr pro 1530 GGA GCA CCG AGC ACA GAA GCA TCA GGC CAG ACT GGG CCT CAA GAG gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu CCC ACC TCC GCC AGG GCC TAG AGA GCC TGG TGT TGG GTC ATG CTG 1575 pro thr ser ala arg ala \*\*\* GGA AGG GAG CGG CAG CCC AGC CAG GCC TGG CCC ATA AAA GGC TCC CAT GCT GAG CAG CCC ATT GCT GAA GCC AGG ATG TTC TTG ACC TGG 1665 CTG GCA TCT GGC ACT TGC AAT TTT GGA TTT TGT GGG TCA GTT TTA 1710 CGT ACA TAG GGC ATT TTG CAA GGC CTT GCA AAT GCA TTT ATA CCT 1755 GTA AGT GTA CAG TGG GCT TGC ATT GGG GAT GGG GGT GTG TAC AGA 1800 1845 TGA AGT CAG TGG CTT GTC TGT GAG CTG AAG AGT CTT GAG AGG GGC TGT CAT CTG TAG CTG CCA TCA CAG TGA GTT GGC AGA AGT GAC TTG 1890 AGC ATT TCT CTG TCT GAT TTG AGG CTC AGA CCC CTC CCT GCC CTT 1935 TCA GAG CTC AAA ACA AGT AAT ACA CCA AGG TCT TGA CTG CAT TTG 1980 TCT TGT GAG CAG GGC TTG CTT GGT CAG CTC AGG CCC TCC TAG CTG 2025 CTT GGA GGC TCC TTT GAT TCT CTA GAC CTG GAA AAG GTG TCC CTA 2070 GGC AGA GCC CTG GCA GGG CGC TCA GAG CTG GGA TTT CCT GCC TGG 2115 AAC AAG GGA CCT GGA GAA TGT TTT TGC GTG GGA TGA TGT GCT GGT 2160 2205 CAG GAG CCC CTT GGG CAT CGC TTC CCC TGC CCT TTG GTA GTG CCA GGA CCA GGC CAA TGA TGC TTC TCA GTA GCC TTA TCA TTC ACA GGT 2250 GCC TCT CTA GCC TGC ACA AAT GAT TGA CAA GAG ATC ACC CAA AGG 2295 ATT ATT TCT GAA GGT GTT TTT TTC TTT ATT TCT TTT TCT TTT 2340 TTT TTT CTT TTT TTT TTG CAC ATG ACA GTG TTT GTA TTG 2385 AGG ACC TTC CAA GGA AAA GGG ATG CTG TAC CAG TGG TGC CTG GGT 2430 GCC TGG CCT CCA GTG TCC CAC CTC CTT CAC CAC CCC ACT TGG CTC 2475 CTT TGC CAT CTT GAT GCT GAG GTT TCC TGT TTG GTG AGA TCA GGT 2520 2565 TGT TTG TGG TAA AAG AAA GGA AAG GGC TTC TGA TGG CTT TGC CAC AAG CTT ACC TGT GGG TTT CAG TCC TGA GAG GCC ACC ACC AGT TCC 2610 CAT CAG CAC TGT CTC CAT GCA GCA GTT GCT GGG TCC CAT GTC CAG 2700 . CTG CCT TGG CTT CAT GGG TTT TTC TGC TTC CTG CCC CCA CCC CCA CAT GTG CAA TCC TCA AGA TTT GTC CTG ATT CTA TTT CCT GGC 2745 ACC TCC CTG CCT GTC CTT GGG GAT TCT ACT TCT TCC TGT GTG GGG 2790 2835 CCC ATA GCT GTT GTC TAA CAG GTA AGA AAT GAA ATT GAA CTA TTG ACT GGG CCC CAG AAA TCC ATA AAA TGG CTG CAG ACA GTT GTT TCT 2880 2925 GTG TCC TGT TCT ACC CCC ACT CCA GTA CAT AAC TAC TAT GTA CTG 2970 TGT AGA GCC ATT CTA TAT GCT GAA TGT TCT GCT GTT GCA AAC TTG CCA GGG TAT TAG CCA GTG TTT GTG CCA AGC AGT TTT CGG GGA CAA 3015 CAG AAT GAC TCA GAC CAA GAT GGA TAG GAT GGT TAG GGC TTT GCT 3060 TCT TGC TGT TTT TCT TTG AAC TAG TCA TTG TCC TGC AGG TCC CTT 3105 CAT CTT CCA TAC CTA GCC CAC TCT TTT AGC CCT TAC CTT AAA TCT 3150 3195 CTC AGA TAA GTT GGT TCA CAA AGA ATG TTA AGT ACT GAA TCA TGT GTG ACT GAG ACC AGA GAT GGC AAA TGA ATG GCA CAC CAT TTC TCC 3240 TTC TCC TGC CCC AGG GCA GGT ACC ACT GAT CTG CAT CAG AGT TGC 3285 CTG CTA TTC TCT GGT GTA TCC TTC ACA TCT AGG TGC CCT CAA GCA 3330 GCT GTG TGA GTG TTG AGA TCT CTG CCA TCT CTG GCT GAG ATA CTG 3375 CTG TCC TGT GAA GTG TTT CCC ATG ACC TTT TTC TTC CCC TTT GAA 3420 TCC CTC TTG TCT GGA GTA GTC CTT GCC TTC TTC TTG CTC CAG TAG 3465

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GCC TTT TCC TTA CCC CAG CCC TTG TGC CAG GCT AAG CTG GTA CAA
3555
      GAG CTG CCA ACT CAC AGA GTT TTG CTA GGC GAG AGA GGT GCA GGG
3600
      AAG AGG CAG AGG TAT GCA CCT TCC CCC TTG AAG AGA GGG GAA AGG
3645
      CCT ACA GTG GCC CAC ATA ATT GCC TGA CTC ACA CTT CAG CTA CCT
3690
      CTT AAT GCC TGT GGA GGG ACT GGA GCT GCT GGA TCC CAG TGT GGT
3735
      GGT GTA GGA GGC CAC AGT GAG CAG GTG GCC CCA GCT GGG TTT CCC
3780
      AGG TCA GGA ATG TGG GCC CCA GGC AAG GTG CAG CCT TTG CTC ACA
      GCT CCA TCC ATG TCT AGA CCT TCA GGC CAG TCT GCA GAT GAG GTT
3825
      CCC TAC CTT TTT CTT CTC TTC ATT GAC CAA ATC AAC CAA TCA CTA
3870
      CAG CTG CTC TGC TTC TGC TTT CCA AAG TAG CCC AGG TCC TGG GCC
3915
3960
      AGA TGC AGG GGA GGT GCC TAT CCA TGA GTG AAG GCC AGT GTC TTC
4005
      CTC ACC TGG GTG GTC CCA CAC TTG TGA CCC TCA GTT TTA GGA CCC
4050
      AAG ATC TGT GGT TTC TTA GAT TGC TAG CTT TTC CTC CAG GGG
      ACC ACA GCA GGT GAA GCT CAA GAG CGC ATG GCT CTG CTA ATA GTA
4095
      AAT TGT TTT CAG GGC CTT GTC CAG CTG AGA GCT TCA TGT CCA CCA
4140
4185
      GAT TCT GAG AGG TGT CAG CAC TTT TTT TTT TTA TTT GTT GTT
4230
      TGT TTT CCA TGA GGT TAT CGG ACC ATG GGC TGA GCT CAG GCA CTT
4275
      TCT GTA GGA GAC TGT TAT TTC TGT AAA GAT GGT TAT TTA ACC CTC
4320
      CTC CAC CCC ATC ACG GTG GCC CTG AGG GCT GAC CCG GAG GCC AGT
4365
      GGA GCT GCC TGG TGT CCA CGG GGG AGG GCC AAG GCC TGC TGA GCT
     GAT TCT CCA GCT GCC CCA GCC TTT CCG CCT TGC ACA GCA CAG
4410
4455
     AGG TGG TCA CCC CAG GGA CAG CCA GGC ACC TGC TCC TCT TGC CCT
4500
     TCC TGG GGG AAA GGA GCT GCC TTC TGT CCC TGT AAC TGC TTT CCT
      TAT GGC CCA ACC CGG CCA CTC AGA CTT GTT TGA AGC TGC ACT GGC
4545
     AGC TTT TTT GTC TCC TTT GGG TAT TCA CAA CAG CCA GGG ACT TGA
4590
     TTT TGA TGT ATT TTA AAC CAC ATT AAA TAA AGA GTC TGT TGC CTT
4635
4680
     AAA AAA AAA AAA AAA
```

FIG. 17D

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GTG GAC GTG GAT GAG TAC GAC GAG AAC AAG TTC GTG val asp val asp glu tyr asp glu asn lys phe val GAC GAG GAA GAC GGC GGC GAC GGC asp glu glu asp gly gly asp gly

FIG. 18

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	1				50
Rabbit				GDGQAGPDEG	
Human	• • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	•••••	
	51 .				100
Rabbit	MTAALQAALK	NPPINTRSQA	VKDRAGSIVL	KVLISFKAGD	IEKAVQSLDR
Human	• • • • • • • • • • •	K	•••••		K
	101				150
Rabbit				KALAAGGVGS	
Human	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	M		• • • • • • • • • • • • • • • • • • • •
	151				
Rabbit	v		FIG. 19	a	
Human	•		110.13	ט	

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	1				50
Rabbit	EERVLEKEEE	EEEEEDDEDD	DDDVVSEGSE	VPESDRPAGA	QHHQLNGGER
Human	• • • • • • • • • • • • • • • • • • • •	.DDDEDEE		•••••	
	51		•		100
Rabbit	GPQTAKERAK	EWSLCGPHPG	QEEGRGPAAG	SGTRQVFSMA	ALSKEGGSAS
Human	sv.	TPQ.	.DP.		.MNT
	101				150
Rabbit	STTGPDSPSP	VPLPPGKPAL	PGADGTPFGC	PAGRKEKPAD	PVEWTVMDVV
Human	VA	• • • • • • • • • • • • • • • • • • • •		.PS.	• • • • • • • • • •
	151				200
Rabbit	EYFTEAGFPE	QATAFQEQEI	DGKSLLLMQR	TDVLTGLSIR	LGPALKIYEH
Human	• • • • • • • • • • • • • • • • • • • •				
	201	220			
	HIKVLQQGHF				
Human		D	FIG	. 20	

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Rabbit Human			· · ·	QGRPGRPAPA .ESQA	- ~
Rabbit Human				DILSTYCVDN	
Rabbit Human				NGEKETSKAE YPGD	
Rabbit Human	151 EVGDRDHRRP	QEKKKAKGLG	KEITLLMQTL	NTLSTPEEKL	
Rabbit Human				EHSKAILARS	-
Rabbit Human				TLNDIQLQME	•••••
Rabbit Human		KKLIEQYELR	EEHIDKVFKH	KDLQQQLVDA	•••••
Rabbit Human		DFLLKEAVES	QRMCELMKQQ	ETHLKQQLAL	
Rabbit Human		TFKQEMEKMT	KKIKKLEKET	TMYRSRWESS	•••••
Rabbit Human				DLNKRVQDLS	SLT
Rabbit Human				TDASCCAGAP .E.P.YP	
Rabbit Human	551 QEPTTATA S.R.	F	IG. 21		

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1	AAGCTTTATAAAGATTTAACTACCTAATAAGGTAGAGAAGTAATTTATGTGCCCACTAAA	60
61	AAATACTCAATTTCTGAATGTTCGTCCAAAATTAACTTGTCAGATCATTAAATCATTGAC	120
121	TAGAAACACGTTGAGTACCTATTATGTACTAGGCACTTAGATCATTGTGAGACAATAAAA	180
181	AATACTGCATTAGAAAAGGACATTTTTCACATCTTAAATGCAATAAGCATTATTTTGGCTG	
	GCAGTTAATTACATTTAACACATTTTTCACATCTTAAATGCAATAAGCATTATTTGGCTG	240
241	·	300 .
301	TTATACCCTTGAGCAATCGATTATTTAAATTTCTTTCACTATTCCCTTAAGCTGATTTCT	360
361	ACTCTGGGATTCTTTCATAGTTCTCAAATAAGAAAATAAAAAATTTCCTAAATAAGGCAA	420
421	TACAAAAGAATAGAAATGTAAGAGAAGAGATATATTAGCTCTTGAATCCCTGTTTCCATT	480
481	TGCTGTCAATAGTGCCTCTAATGTTCGATTTTCTCTTCAAAGAAAATCTTGATTTAAAA	540
541	GGAAGAAAAGTACAATCACCTTTAACAGCTAAAGTATACTGATTAGCATCTACTAAAGT	600
601	TAGCAAAGACTGAAAAAAAAATTGTAAAATCTTTATTCTAAGTTATATAACGCCA	660
661	TTCACCATAGTAATGATTTTATACTTTGGTATATGGCTTTTTAAAATAAAT	720
721	AGGTAAAAATTTTTCCTTTGCTGTCTTAAGGCATTCCTAAGAGAATTTTTACCAGTGTGT	780
781	GTTCATAACTTGAATGTTAATTTAAACAATGTTACTTCTATCACCTAAATGATATACTTA	840
841	TAGAAGAGTGGTTTAATTGGGAACAGAAAAACACCACATTGCTTCTTCCCAAGAAAAAGG	900
901	GATGTATTCCATTCTCGAGGTCTCTCTCCCACTCTCTATTTATATATA	960
961	GATAAATATACACACATTATATATGTATTTTTTTGAACTTAAAGAAGACTGGACATATGT	1020
1021	ATTTACATGTATATATCCAACAAATATTTAATTTTGAGATCTCTCTC	1080
1081	ATTATTCTCAGTATGAATTCTCAAACTGTACGGTCTTTCACATTTCATTCA	1140
1141	CATGTATCGAGTCCCTTCTGCATGCTTAGCTTTTTGTCATATGGAAGGAA	1200
1201	AAAAACTGTTTCTGCCCTTCAGAATCTTTCCATCTCTTCTAGGAAGGA	1260
1261	TATATCATTAAGAAATTTATAAGACTAGTCCCAAAACCAATGGTACAAGCAACATGCATT	1320
1321	TTACATTTATGTAGAATTTTAGAGCTTGGAAACACTTTCGTGATATATAATCCTAAGAAC	1380
1381	AATCTTGTAAAGTGCACATTATTAGCTCCATTTCAGTGATGAGGAATCTGAGACAGAATT	1440
1441	TTAAGTGACATGTCTCGTTCAAACATTATGAGTGGAAGAGTCAACACTTAAGCCTGAGTT	1500
1501	TTCTGATTCTAAGCCTAGTGCTCTTTTCAACACAGCACTGGAAACCAAAGATTGTGGTAC	1560
1561	ACAACAAGGCAACAGCCAGTCTTCTTGCTCGAGGTCCAACTAAACTGGACCCATACCGAG	1620
	CAGTGTCCAGCCAAATGTCCAAATTAATTTTATCCTGCAAATATTTGTTCTTCAGTGTAA	1680
1621	TACACACACCACACTACCATTTCCTTCGTCTTAGTGCCTTTATCTCCTACATTCCAGAA	1740
1681	ATGGGGATGTCAAATATTTTTTTAAATCTGGCCTAGATGGAATCATATAAATCTCAGAAT	
1741		1800
1801	ATAATATAAATCTTAAAGGTCTGGTTTCCACCAATCCTTCCACATTTTGTTTTCCCCCAG	1860
1861	CACTAGAGAGCCTAACCTACCCTCACCCTTTCGAGCATTCTTGCTCCAAACGACCACCT	1920
1921	ATTTTAAGATGTCAATGACCCTTTCCCAAATTCTACAAATTCACCCCAGTTTTGCCACCC	1980
1981	GACCCCAGCGCCTGCCCGGACACGTTCCCCTCCCTATAGATTTGATACCGAGTTCA	2040
2041	GGTTCTGCAGATCCCGTTGCGATGCTGTCACACAGCACTGACAGATAAGATTTGACCTTT	2100
2101	CGACTCCGTCCTTGGGGACTTCCCGCTGGCCAAGAAGGGTAGTTCCAATCCCAGGAAACG	2160
2161	GGCTTCCTGCTCAGGAACGCAGCCTCTAGCAGCGCACAGTCTGAGGCAATGTCTCCGGCA	2220
2221	ATTAGAACGATGCTGGGCGCCCGGGTGTGCATCACTCTGCCTCATACTCCTACCAACTGC	2280
2281	AGGGCACTCGGTCCGGCAGCCAGTCCATCCCACCCACACCCAAGTCCCAGCCAG	2340
2341	CTTACGCAGGACCCCGATGATAGGTCGTTGACGGCTGCAGCAAAAGCCAAGGCCACCTGC	2400
2401	CGCTGCTGCCCATCCCCGCCAATCTGAGACCCCCTAGACTGGACCGCAGAAAAGCGTTTC	2460
2461	TATGGGAACCCCCCACCGAGAATCACGTGACGCAATCGGACGACCAATCGCTTCTTACC	2520
2521	TCTGCCCGCGGTCCAGCTTTTGGCCCTCCCTCTCGCCCCGCCTCCTTCGCCCAGCCCCG	2580
2581	CCCCTTGCCTGCGGAGAGCCCGCGCCTGCGCGCTGTGTCCTGCGCGCTCCTTCCCTCGCG	2640
2641	CGCGCTCTCCGTGGAAGAGCAGGGGCAGCGTGGGAGGCGCCAAGGGAGCGCGAACCTGAG	2700
2701	GAGGAAGAAACGGGGCTAGCGCGCAGGCCCAGAACGGTCCGAGCCGCGGCAGTCGGCGAC	2760
2761	GCCTCAGAGCGGAAGAGGGAAGTGAATCAGGCGCCGGGTAGTGGGTTGCTGGGCTGGGCT	2820
2821	TGCTGAGGTAGAGGCGCCAAGAAGAGGCCTTTGCCGCTGGTCGGGATTGGGATGTCG M S	2880
2881	AAGAACACAGTGTCGTCGGCCCGCTTCCGGAAGGTGGACGTGGATGAATATGACGAGAACKNTVSSARFRKVDVDEYDEN	2940

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2941	AAGTTCGTGGACGAAGAAGATGGGGGCGACGACGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGAGAAGA	3000
3001	GACTCCTGCCTGCGGCAATATCCTTGCATTCACCGCCCTCCCCACCCCAGCCCAGCCCAG	3060
3061	CCCGCCCTTCTCCTGGGACCCGGGAGCCTGCAGGATCCGCGGGGCACCGGCGCGGAGCTG	3120
3121	CCTCTCAACCTGCGGCTTAACCTGTCTCTTTGGGATCGCCCGCTCTGAGAGGGCAAGGGG	3180
3181	GAAGCCCCCGTTTCCTACCCAGTCGGCAGGAGACGCGAGGGTCCCACTCTTGGAAGCCTG	3240
3241	CCCTACCCGCGCGCCTTCCACGCCCCCAGATTCCTCAGGTTGCACCCGAGTGCCTGCC	3300
3301	GCCTCGGGAACTGGTCCCGCCGCCCCGCGCCCTCGCGGCGCTGGGGAAGGCGGCCCCGGCT	3360
3361	GGTGGGGAAGGCTGGTGCCGACCGCCTTAGTTTTTCTTCCTAGAACTCTGATTTCCTGGG	3420
3421	GTCACATTAGCTCCAGAAATTTCTGATTGTGGGGAACCTGCATCTTTCCTTAGTGGTTTT	3480
3481	GTTTTTTGGTTGTTTTTTGTTATTGGTAGCGTTAAGGTAGTTTATTGCTTACCGGGGGG	3540
3541	CCGGGGGAGATGGGACTGTTCGAAAATTGAGGGTCCCTGTGCTTTCAGCCCATTGGCCTT	3600
3601	TTTAAAAAAAAAAAAAAAAAGAAGAAGAAGAAGGGGATTTGGCAAAATATACATTGTACAG	3660
3661	AATTTGTTAACTGGGGGAGGGAATGAATACAAAAATACAAAACTCCTAGAAGGAAG	3720
3721	TGGAGCCTTTTACCTGCTAAGAAAAGGACAATAGAAAAAACAACGGGGAATGCGTGTGGA	3780
3781	GAATCCTTGGAAATATTTAAAATAAACCCCAATGAATAAGATAGAAGATGAGTCATTCGT	3840
3841	ATAAAGCAGAATCATTTTTGTAATCCTAAAATTGTTTCCATTTTAGTTAAAATATGGCAG	3900
3901	TCAGTTCCCGGTTTCTGTTTTTGCATATTTGAATATTCATAACTTTGGCTTCGCATTTGC	3960
3961	ATTACATCTTTTTTAGAAAAATGTAAATGTTGCAAAAAAACCGAAGCTGTAGTTTTAGAA	4020
4021	AATCTCAGACACTGAATTTGTATGCATTTCTAATTCTTGGGTGTATTCATAAGGAAGACT	4080
4081	CTCAACAATGTCCTGTTATAGTGGGGAAATATGAGAGTGAAAATATTTAATGGCAACAAT	4140
4141	ATCCTTTTTTAAAGGCACCTAAATAGAGCATTAGACATTTATCAATATATAGATAG	4200
4201	TTGCCCAACTTTCACAATTAATTAGCTGTTGCTCTTTTGCATTATTTAAATACTTAAGTG	4260
4261	CTTGGAGTTATAAAAAATGAGCTAATCTACATCAGGCATGCTTCTCTAGAAATCCCTGCA	4320
4321	GCCTTGAAAATAACAGCTTGTCAACCAGAGATTTTGTGTAAGAACTTTTTCTTTAGAAAA	4380
4381	TAAATGGTGAACATGCTTCCTAAAAACATTATTTGTGATGGGATAAGATGGTGTTTTATG AAACCCCAGTGTATTTTAGGTAATTTGTGGTGACTTTTAAAAGGTACTGCTGTATCCATA	4440 4500
4441	TCAGTGGATCTGCTTTTTGATCAGTTCATCTTAAAATATAAAGGTACTGCTGTATCCATA	4560
4501 4561	CGTTACATACAGCCAGGAAAGACAGCCCTAGTGGTGGGGTACTAGAGTTGGAGGAACAAG	4620
4621	TGAACTCTGTGGTTTTCCTTTTAGGGGAATGTTTGTACATTCTGACAGTCTGATTGGCCT	4680
4681	TCTGTTTCTCATGCTTGCTAACTCACTAGTGCTTTCAAAGAGAGCCTGAATTTAATAGGT	4740
4741	ATGGTCTAACACAGTTTGAATAACCTTTGTGAAATATGAGAGAAAATATCTAAAGCAAAA	4800
4801	AATTAAGCTGCCACCTAAGGGACATATGAATTATTACATCTTCTGTGATGCCTCTTTTCA	4860
4861	TCAATATTGAGAGATTGCTAATGTGTATCATTCAGATTGCTAATCTGCCAGCATGTTCTA	4920
4921	CCAGCATTTCAGATAATACAGAATATGGTTCTAGCAAAAGTTTGGTCTTTATTTTTTCAA	4980
4981	TTAGAATCACAGGAAAAGACATATTTTGGTTGATAATAGGTTATTTCATTTGGGGGACTA	5040
5041	ATAATTCTGATATATTTTTAGGATTTCTTTAACACCACTCTAGGTAATGTTTGCATATG	5100
5101	TATCTCACTGGGAAATGAAAGACTATCAAGGTGTTCACTTGATAGTTAGAACCAAGGGTG	5160
5161	AAACAGTCTTTGCTTTATTAAAAAAAAGTCTAATGTTCTATTTTGCTTTTGATATTTTGC	5220
5221	CTTTGATTAACATCCTGGAAACCAACACATTGAATTTCCAGTATTGAACATAGTGACCAA	5280
5281	AGTAATTTTCTTTTTATATGTAAATCAAGTCATAAAGAACCAGTGGTTATAATGCTTTCT	5340
5341	GGGGGCCATCCTTTGCTGTTACACCCTTAACTTCCATCACAGGAAACATGACAGCTGCCC G N M T A A L	5400
5401	TACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAGAGTCAGGCAGTGAAGGTGAGTC Q A A L K N P P I N T K S Q A V K	5460

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5461	GCAGACTACAACACAGTGATCTCTGCTGATATCTTATTCTTAGTAAAATCCTTGCAGTGC	5520
5521	AAAAAAAATCAATATTTTAACTGTTTGCTATCTTTGACAAGAAGAGTTTATAATGTAGT	5580
5581	TTGATAGGTAAAAATTTCACGTGAAAAAATAGCCCTATAATGTAGTTATGATAATGCTGC	5640
5641	ATGGTAAGATACAGTAAGTTCAAACGATAGTGAAATCATTTGTGTGTG	5700
5701	ACCACTCAGGCTGAATTTGAGCAAAGGTTTGAAAAATAAGTTAAACCTTTACAAAAATAA	5760
5761	ACAGATTGTAATTGCTTTTTAAAGATTTTTTAAAACCATACAAATACTAAATACTTATTA	5820
5821	TAGAAAGCTCAGACATATGAGAAGGTTAAAAAAGATAGTGGTTTGTGGTCCCAGCACCCAG	5880
5881	AGATAACAGTTACTACTTTGGGGCCTTGCTGTATTGTTACAGAGTTCCCTTTTGTTTTTT	5940
5941	TAAGAATGAATTTTTAAAACGGGCTTTTTCAGCTATATGCAATGGTACATGAGCTTTCCT	6000
6001	TCCCCAATAAGTTAATAGCCTTTTTTAACACTTGTATATGGATAAGCTCCAGTGTATACA	6060
6061	TAACTAATCTTTTGTTTATATTTAGACTGACTTTTTTTTT	6120
6121	TCAATATTTTTTGGTAAATTTTTAATTGTTCTCTTTTGAGTAAATTGCTAGCAGTGAATTA	6180
6181	CTGGATCAAAGAATGCACTTTTTTTAAGGCTTTTGGTATGCAGTATTGCCAAATTGCCC	6240
6241	TTCAGAACAGTTGTGCAACTTACATTCTCTGCAGTCTTTTACTAATTCTTAACCTATTTA	6300
6301	CGTATTTATTTAAAATGATGCCCATAGCATCAACCCCGTTGTCCATAGCTATTCATACAT	6360
6361	CCTAGGAGCTTCAAGAATCTCAATTGAATAGTAGTAAGTA	6420
6421	ATAATTATCTAGGTAACATAATTTTTTATTGGGGAAAATTTCTTTGGTTTTTACAAGTTG	6480
6481	TAAAGATTGTCGTTGAAATTTCATTTTTACCGTGGATGCAAAGATATTTTTCTAAATCTG	6540
6541	GTAATTGCAGTCTTTAAACCAAAGATAACAGTAGGTGGTAGAAACATTCTGTGAAATCCT	6600
6601	GACCAGTAGGAATGCTGGAGGTATCACTTTGTGTTGAATGGAAGGAGAAACGAATTGTTG	6660
6661	AAAAGGTCAGTTAAGTGTTTCCTTTGCTTGGCCGGATGGGTAAGAAAATAACTGCTTTTG	6720
6721	AAGCAGGCTTTTGCCAAAGAAAAAGATCATTATTAATGAACATCACTATATTTCATATC	6780
6781	TACAGTCAATTCATATAAATTACAGTCAATTTTCTTTTAAGACAGCTTGGTTTATTAAAA	6840
6841	TTTTTAAATAAAAAGTTTTTAAGAAAAATTACTTCTGAAGGATAATTCAAGGTGAAAC	6900
6901	TGCAAATCTGCCTCCTTGTTTTGTTGGGAATTTTTTTTTT	6960
6961	GAGTCTCACTCTATCACCCAGGTTGGAGTGCAGTGGTGCAATCTCAACTCACTGCACCCT	7020
7021	CCGCCTCCCGGGTTTAAGCAATCCTCCTGCTTCAGCCTCCCGAGTAGCTGGGATCACAGG	7080
7081	CACACCACCATGCCTGGATAATTTCTGTATTTTTAGAAGAAAACAGGGTTTTACCATT	7140
7141	TTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCTGCCCATCTCGGCCTCCCAAA	7200
7201	GTGCTGGGATTACAGCTGTGGGCCACCACACCCGGCCGTTTTGTTGGGATTTTTTTT	7260
7261	TAAGATCAAGACATAAATTTAAATGTTGTTTTAATAAATTGTTAAAATTATCACATTGATC	7320
7321	TGTTAGCAAATCCTCTCAGCTCTGCCTTCAATTATGTTAATAGTCTGTCAAGTTTCTTAC	7380
7381	CACCTCCACTGCTACTATGCTTACCACATCCAGCCTGTATTATTGCAATTGCCTCCTAAT	7440
7441	TGCTCTCCCTGCTTCTACCTTATCCCCTACTCCCACAGCTTATTTTCTGTAACATAGATG	7500
7501	CCAAAGCAATCCTGTTAAAATGTGAGTCAGATTATGGCACTGCTCTTAAAACCTTCCAAT	7560
7561	GTCTTCTCATTTCTCTCAGTAAAAGCCAAACTCCTTACAATGCCTGTAGGCCTTACACGA	7620
7621	TCTGTCCTCCCATAACCTCTGACTTACTCACGTGCTTTTCTCCCACCAATCCACTCCAAC	7680
7681	CACATTGGGTTTTTTTCTGTTCCTGGAACACACTGAACACACAC	7740
7741	TCCTCTGTCTGAAACACTTTCCTCAGTTATCCCAAGCCTTCTTTCACGTCCTTCAGGTCC	7800
7801	TTACTCAAATGTCACATTCATAGTGTAGACTTTCTGAAATTCTAAACCCTCCTCATACAG	7860
7001		
7061	, m, m, m, m, m, n, m, c, m, c, m, c, m, m, m, m, m, m, c, n, c, c, c, n, c, c, c, n, c,	7920
\86I	ATATGTCTAAATGTTCTGTTATTTATTGACCCACCAGGACCGGCAGGCA	1920
7921	GAAGGTGCTCATCTCTTTTAAAGCTAATGATATAGAAAAGGCAGTTCAATCTCTGGACAA	7980
	K V L I S F K A N D I E K A V Q S L D K	
7981	GAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCGTCTGACAA	8040
	NGVDLLMKYIYKGFESPSDN	
8041	TAGCAGTGCTATGTTACTGCAATGGCATGAAAAGGTAAGTTATGAATTATAAATCTATAT	8100
	S S A M L L Q W H E K	
	· · · · ·	
	FIG. 22C	

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8101	GACTGGTTCTTTTACAATAGGGAATGACAATGACAACCTCTCTCACCTAAATAACCATTT	8160
8161	TGATTTGTTGTACATTTTTGTTATTACAAATAAAATGCATGAAAAGGATAGTTCATATTT	8220
8221	ATGTTTACTAGCCTTGGTCTTAAGAGATTCTGATTCCAACACTTGTGTTTATTCAACAAT	8280
8281	GATTATTAGTAATTAAACATAATCTTGAACTCTGAATTAAATCAAAACTTTGTAAAAGAA	8340
8341	AATAAGCAATACAAATCAAGAATTCTTTCACAGTGACCAAAAGGTGAAAACAACACAAGG	8400
8401	ATCGAATATGATTCAACCA	8419
8420	TTAAAAGGAATGACATTCTGACACATGCTATAACATTAATAAACCTTGAAAACATACCAA	8479
8480	GTGAAATGAGCCAAACACAAAAGAACTAATATTTTATAATTTTACTTATATGAAATAATC	8539
8540	TAGGATAGGCAAACACAAAGGGACAGAAAGTCCTTAGAGGTTACTAGGAAGTAGGGAAAG	8599
8600	CAAGGAATAGGGAGTTAGTGCTTAATAGGTACAGAGTTCCTCCTTGGAGTGGTAAAAAAG	8659
8660	TTTTGGAAACAGATAGTGGTGATGGCTACAGTACATTGTGAATATAATTAAT	8719
8720	ATTTTACACTTAAAGATGGTTAAAATGGCAAATTTTGTGTTAGATATTTTACAACTTTTT	8779
8780	TAAAGAATTAGGAGTTTGGAGGATCAAGAATTCTTAAATCATGTTTTTCTATTTTCATGT	8839
8840	GTATATTTTGCAATGTAAGTAGATGCTGGTACATCATCTGTCAAAAGAGTATAAGTGATT	8899
8900	TTGAGCTTTGGGTAAAAAACTGGATAACATGTAAATAGAACCAGTCATAAAAATATTGAG	8959
8960	TGTTTGAAGTGTATCTGAGTGAAAACACAAACATAAGAAAAAAGCACATAGTAAAACAAT	9019
9020	AGTTCCCCCTTTTACTCTAAAATGCACCAATTTGGGTAGTAATTTATATGGCACCCTATT	9079
9080	CATGGAACACTTTCTGTTGCCAGGTACCATACTATTAATGTTTTATTTA	9139
9140	AACCCTGTGGAAGTATATAAATATCTTTATCATCCTCAATTTACAGATGAAAAGCTAGCT	9199
9200	TTAAAACCCAAGCCAGCGTAGTTCTAGCATAGCCTCAAGATTGCAGTGAACATTGATTAC	9259
9260	TTATTATATTCCACATATTCTTCAAAGGACTTTATAAATATTAACTCATTTAATCCTCAT	9319
9320	AAAAATGGAGGGAAATGCTTGCTATTATTCCTCTTTTTGTCACTGAGGAAACTGAGGCATG	9379
9380	TGTGAAGTCTTCATTTCTTCCAAATGTCAGTCACCAGTTTTTACCAATCTTCGAAGTATT	9439
9440	TCTGAAATCTATCTGTTCAAGCGTATCTAATGCAGCTGTTCACAGCATCTCTCCCAGTCT	9499
9500	GTTGCCATAGCTTCCTGACTGGTTTCCCAGTTAACAGTTTTGCCTCCTTCAAATCTGTTC	9559
9560	TCCACCCAGCCATCAAAATGATATCTTTAAAATCAAAATTGCCCTTGTCAGTCA	9619
9620	GGGATAAAGTCAAAGTTCCCAAGTCTAGCTTCATCTTCCATGTCATTCTTCCCCTCAGGC	9679
9680	TATAGCAATGCCAGCCTTTTTCCTGAATGCACCATATTGTTTCACACCTCCATACATTTG	9739
9740	CTCATGATTTTCTGGTGTTAGCCTGTCACCTACTCATTCTTTTAATGTGTCATTTCCTCC	9799
9800	ATGAAGCCTTAGCTGAAACATTCCTCTATACTGTTAATCTGGGTATAAGCCTCTCCCTGG	9859
9860	TGCTTTAATAGCACCTGCAGCACACTCTCATTTCATACATTAGATTAAAATTACCTGTT	9919
9920	TATATGTCTGTCTCCTCATGCTAGACCAGAAAATGCTGTATTTGTTCACTTTTGTATCCC	9979
9980	CAGCATCTAGCACAGTACTCAGTATACAAAGGTATTCCATAAATATTTTTTGAACAGAAA	10039
10040	GAAACCAGAGCTCAGATTCCTAATACTTGATCATTACTCTCTATTTTTCAAATTAGAGTC	10099
10100	AGAGTTAAAGTTTCTAAGTTCTTAGCTATTAAACAATACCTTCTTTCT	10159
10160	AAATCTGACAAAGGCTGACTAATCGAAGTGGAAGTTGGGATGGTTGATCCCAGTTTGAAT	10219
10220	TTTCTTCTGACTATGTGGTGAGAATGAGAAATGCAGAATGTCCACCTGTTTTGAGCAGGA	10279
10280	ACACTATGCTGCAGATTTTTTTTTTTTTTTTTTTTTTTT	10339
10340	TCTGTCGCCCAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCCTCCT	10399
10400	GGGTTCACACCATTGTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACCCGCCA	10459
10460	CCACGCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTAGCCAGG	10519
10520	ATGGTCTTGATCTCCTGACCTCGTGATCCGCCGGCCTCGGCCTCCCAAAGTGCTGGGATT	10579
10580	ACAGGCGTGAGCCACCGCGCCCGGCCTATGCTGCAGATTTTTTAAAACATTATTTAGAAT	10639
10640	TAATGTACTAAAATGTAAACTAGTATCTCACTAGAATGTAACTTCATGAGGGCAGGGACT	10699
10700	TTCAAGGTTTTGTTTATTACTGTAACCTCAGTGCCAAGAACAGTACCTGGTGCATAATTG	10759
10760	GTGCTCAAGAATTTATTATTTGTTAACTAATAAATTCAGGGTCTATAGCAGTGCCCATTC	10819
10820	CTTCTTTAAGAAAATGTTTTACCAAATATGAGAATTGACCTTTTATTATTCTGTCAACA	10879
10880	TTTACATCCTGGTTTGTTTTTAGGCACTTGCTGCTGGAGGAGTAGGGTCCATTGTTCGTG	10939
	A L A A G G V G S I V R V	
10940	TCTTGACTGCAAGAAAACTGTGTAGTCTGGCAGGAAGTGGATTATCTGCCTCGGGAGTG	10999
	L T A R K T V *	
	FIG. 22D	

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11000	GGAATTGCTGGTACAAAGACCAAAACAACCAAATGCCACCGCTGCCCTGTGGGTAGCATC	11059
11060	TGTTTCTCTCAGCTTTGCCTTCTTGCTTTTTCATATCTGTAAAGAAAAAAATTACATATC	11119
11120	AGTTGTCCTTTAATGAAAATTGGGATAATATAGAAGAAATTGTGTTAAAATAGAAGTGTT	11179
11180	TCATCCTTTCAAAACCATTTCAGTGATGTTTATACCAATCTGTATATAGTATAATTTACA	11239
11240	TTCAAGTTTAATTGTGCAACTTTTAACCCCTGTTGGCTGGTTTTTTTT	11299
11300	TGTATTATTTTTAACTAATACTGAGAGATTTGGTCAGAATTTGAGGCCAGTTTCCTAGCT	11359
11360	CATTGCTAGTCAGGGAAATGATATTTATAAAAAATATGAGAGACTGGCAGCTATTAACAT	11419
11420	TGCAAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATATGTTTTTGGAATAAGTGG	11479
11480	TGGGTGAATACCACTGCTAAGTTATAGCTTTGTTTTTTGCTTGC	11539
11540	TGTGGGTTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCCTCAATTTATT	11599
11600	TGTGGTCACCCAGGGTTCAGAGCAAGAAGTCTTGCTTTATACAAATGTATCCATAAAATA	11659
11660	TCAGAGCTTGTTGGGCATGAACATCAAACTTTTGTTCCACTAATATGGCTCTGTTTGGAA	11719
11720	AAAACTGCAAATCAGAAAGAATGATTTGCAGAAAGAAAGA	11779
11780	ACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTTAGA	11839
11840	CATTATGAGGTATACAACTAGTATTTAAGATACCATTTAATATGCCCCGTAAATGTCTTC	11899
11900	AGTGTTCTTCAGGGTAGTTGGGATCTCAAAAGATTTGGTTCAGATCCAAACAAA	11959
11960	TTCTGTGTTTTAGCTCAGTGTTTTCTAAAAAAAGAAACTGCCACACAGCAAAAAATTGTT	12019
12020	TACTTTGTTGGACAAACCAAATCAGTTCTCAAAAAATGACCGGTGCTTATAAAAAGTTAT	12079
12080	AAATATCGAGTAGCTCTAAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCTTAG	12139
12140	TATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACTGGTGCAGAAATT	12199
12200	CTATAAACTCTTTGCTGTTTTTGATACCTGCTTTTTGTTTCATTTTGTTTTGTAA	12259
12260	AAATGATAAAACTTCAGAAAATAAAATGTCAGTGTTGAATAATTTATTT	12319
12320	TTTAACAATTATGAATGTATGGTTAATTAAGAGGAAAGGTTTTCTGCTTCTACCACCAAG	12379
12380	TACTGTACTCTTAACAAGAACAGTTTGGTAGGGTTTTTATAAGACTATATAGATATAAGA	12439
12440	TGATAGAGAAGAGTCATGAATGATGTCAGAGCACTACTGAAGCCTTTGGAGTGATTCC	12499
12500	ATAGCCTTCTGGATGGCAGCTGAATACCTATATGTAGTATCACTGCCCAAAGACCTAGAC	12559
12560	TAGAAAGTGCAAAGTAGCTTAGCAGCTGCAGTCATTCACTCCCAGCCTCCAAAATTCTCT	12619

FIG. 22E

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1 -
                             GATCCCTCTCCAGGTGGAAG - 60
                                               /11
  61 - CTCCCTTCATACCAAAGTTTAAAGGCCCTGGGGATACGAGTAACTTTGACGACTATGAGG - 120
 121 - AAGAAGAAATCCGGGTCTCCATCAATGAGAAGTGTGGCAAGGAGTTTTCTGAGTTTTAGG - 180
 241 - TGGGAGGGTTGGATTGAACAGCCAGAGGGCCCCAGAGTTCCTTGCATCTAATTTCACCCC - 300
 301 - CACCCCACCCTCCAGGGTTAGGGGGAGCAGGAAGCCCAGATAATCAGAGGGACAGAAACA - 360
 361 - CCAGCTGCTCCCCTCATCCCCTTCACCCTCTCCCCCTCTCCCACTTTTCCCTTCCTC - 420
 421 - TTTCCCCACAGCCCCCAGCCCTCAGCCCTCCCAGCCCACTTCTGCCTGTTTTAAACGA - 480
 481 - GTTTCTCAACTCCAGTCAGACCAGGTCTTGCTGGTGTATCCAGGGACAGGGTATGGAAAG - 540
 541 - AGGGGCTCACGCTTAACTCCAGCCCCCACCCCACCCCCATCCCACCCCAACCACGGCCC - 600
                            Human cAMP-dependent protein kinase
                            catalytic subunit alpha
                            Accession number X07767 (until *)
                            follow arrow until line that
                            begins 1561 -
 1
 841 - AAAGGAGGCGCTGGGGTTTGAACCTCCCCGCTGCTAATCTCCCCTGGGCCCCTCCCCGG - 900
 901 - GGAATCCTCTCTGCCAATCCTGCGAGGGTCTAGGCCCCTTTAGGAAGCCTCCGCTCTCTT - 960
 961 - TTTCCCCAACAGACCTGTCTTCACCCTTGGGCTTTGAAAGCCAGACAAAGCAGCTGCCCC - 1020
1081 - CTTTCCTCCCAGCAGCGTTTCCCCCCAACTCCTTAATTTTATTCTCCGCTAGATTTTAAC - 1140
1141 - GTCCAGCCTTCCCTCAGCTGAGTGGGGAGGGCATCCCTGCAAAAGGGAACAGAAGAGGCC - 1200
1201 - AAGTCCCCCCAAGCCACGGCCCGGGGTTCAAGGCTAGAGCTGCTGGGGAGGGGCTGCCTG - 1260
1261 - TTTTACTCACCCACCAGCTTCCGCCTCCCCATCCTGGGCGCCCCTCCTCCAGCTTAGCT - 1320
1321 - GTCAGCTGTCCATCACCTCTCCCCCACTTTCTCATTTGTGCTTTTTTCTCTCGTAATAGA - 1380
1381 - AAAGTGGGGAGCCGCTGGGGAGCCACCCCATTCATCCCCGTATTTCCCCCCTCTCATAACT - 1440
1501 - GATTCAACCTGTGTGCTGCGAAGGACGAGACTTCCTCTTGAACAGTGTGCTGTTGTAAAC - 1560
1561 - ATATTTGAAAACTATTACCAATAAAGTTTTGTT*TAAAAAAAAGTGTCGCTGGTGTTCTC - 1620 |
1621 - GACTTCGATCACCCCACACACCCCCAGGGGGTTGGAAAGGGAATTTCGGACCCCAGC - 1680
1681 - GTGCAGGCCGATCAGGTCCTGGCTTGAAGTCCTTGTAACCAGGGTTTAGCTGAAATTCCG - 1740
1741 - GCACTCCTTCGGCCCCGCAGGAGAAACGAGCGTCAAACTGCCCTTTGACCCCAGATTCGG - 1800
1801 - GGTCCCCAAATCTGCGGCGCCCCCTCGGCGTCCAGCCCGGGACCGAGAGGGCGCTCTA - 1860
1921 - GGGAGTAGAAGGGGGGGGGGGCGCCCCCCTTCCCGCATCCTCAGCGCCGGGCCAGG - 1980
2221 - CACTCCCCTCCCCCGCCCGCCGCCCGCCCCGCCCCGGCGCCCAACTCC - 2280
2341 - AGCGAGAGCGCAGGGTAAAGGGGGGGGGGGGGGGGCCCGGGCTCCACCTTAAAAGCGGGC - 2400
2581 - GCGGGTCTGTGTGCGTGCGTGCGAGTGAGTGTGTGCATATTTTTTTCTCTCTTT - 2640
2701 - TTTTTTTTTGCAAAGAAACAGCAGCGCCGCCGCCGCCGCCGAGGCGCTGCGCCCCC - 2760
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2821	١ .	- ( -	CGCG	CTG	GGA(	GGG	AGGC	CAGO	CGC	GCAC	CGG:	rgc <i>i</i>	AGC(	CGGC	SCC	GGG	CGGC	GAG		GGC A		; -	2880
2881		- E	CCC	CGG( A	CCC'	P P	P	GCC P	CGG <i>I</i> E	AGA( T	CGG( A	CGG( A	CGGC A	CCG( A	CCAC T	CCAC T	CGGC A	CGG( A	CCGC A	CGC A	CTCG S	; -	2940
2941		- 1 - 5	CGT	CCG( A	CCG( A	CTT( S	CCCC P	GC <i>F</i> H	Y Y	ACC <i>F</i> Q	AAG <i>I</i> E	AGTO W	GAT I	rcci L	GG <i>P</i> D	ACAC T	CAT I	CG <i>I</i> D	ACTC S	GCT L	GCGC R	: -	3000
3001	-	· 1	CGC	GCA <i>I</i> K	AGG( A	CGCC R	GCC P	GGA D	L CCI	GGA E	AGC (	GCAT I	CTC C	CCG R	GAI M	GGT V	GCG R	GCG R	GCG R	GCA H	CGGC G	-	3060
3061	_	· F	CGG2	AGC( P	CGG <i>F</i> E	AGCG R	GCAC T	GCG R	CGC A	CGA E	GCT L	CGA E	GAA K	ACT L	GAT I	'CCA Q	GCA Q	GCG R	CGC A	CGT V	GCTC L	-	3120
3121	-	R	GGG: V	rcac S	CT <i>P</i> Y	ACAA K	G G	GAG S	CAT	CTC S	GTA Y	R R	CAA N	.CGC A	GGC A	GCG R	CGT V	CCA Q	GCC P	GCC P	CCGG R	-	3180
3181	-	C R	GCG( G	SAGC A	CAC T	P	GCC P	GGC A	CCC P	GCC P	GCG R	CGC A	CCC P	CCG R	CGG G	GGC A	CCC P	CGC A	CGC A	CGC(	CGCC A	-	3240
3241	-	G A	CCGC A	CGC A	GCC P	GCC P	GCC P	CAC T	GCC P	CGC A	CCC P	GCC P	GCC P	ACC P	GCC P	CGC A	GCC P	CGT V	CGC A	CGC( A	CGCC A	-	3300
3301	-	G A	CCCC P	:GGC A	CCG R	GGC A	GCC( P	CCG R	CGC A	GGC A	CGC A	CGC A	CGC A	CGC A	CAC. T	AGC A	GCC P	CCC P	CTC S	GCC:		-	3360
	-	P	A	Q	P	G	P	R	Α	Q	R	A	Α	P	L	A	A	Р	P	P	A		3420
	-	Ρ	A	A	P	P	A	V	A	P	P	A	G	P	R	R	A	P	P	P	A		3480
	-	V	A	A	R	E	P	P	L	P	P	P	P	Q	P	P	Α	P	P	Q	Q		3540
	-	Q	Q	P	P	P	P	Q	P	Q	P	P	P	E	G	G	A	V	R	A	G		3600
	-	G	Α	A	R	P	V	S	L	R	E	V	V	R	Y	L	G	G	S	G	G		3660
	-	Α	G	G	R	L	T	R	G	R	V	Q	G	L	L	E	E	E	A	A	A		3720
3721	-	R	G	R	Ļ	E	R	Т	R	L	G	A	L	A	L	P	R	G	D	R	P		
3781	<u>-</u>	GG G	ACG(	GGC0 A	P P	P P	GCC A	GCC A	AGC S	GCC A	CGC R	P P	STCI S	'CGC R	:AGC S	CAAG K	GTG	SAGO	GCG	CCG	GGG	-	3840
3841 3901	<b>-</b>	AG GG	CGG( GAG(	GGC SAAC	GCC	GCG	GCG GCG	TGG GGT	GCA GGC	.GGT :TGG	GGC	GGC TTT	GAA 'GCG	GTT CGC	GGT GTT	GGC TCC	GGG	GGC	GCG CTC	AGT GGT	CCC GCG	<del>-</del>	3900 3960

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4021 4081	- -	TGGTGACCTTGGCAAGTGATTGAATCTCCCGGAGCCTCAGTTTCCTCCGCTGTAAACGCG - 40 GTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTAGTAAGATTTGGTTGTC - 40 GAGGGCTTTAGTTAACACAGAGCCTGGCACGGAGTGAATGCGTAAAAGTTAGTCCGTATT - 41 GTTCTTAAAAGGTGGAATCGGTTCCTCCTCCCCACCGCCCGGACGCCACAGTCAGGGTCTG - 42	080 140
4201	-	GGATTAGAACAGCTACTAATTTTGCATGCTTCTCTCCTCGGCTCCAGAGAGGTGGAGAAG - 42	260
4261	<del>-</del>	AGCGAGTACTTGAGAAGAAGAAGAAGAAGATGAAGAAGAAGAAGAAGAA	320
4321	-	ATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCACCACC - 43 V S E G S E V P E S D R P A G A Q H H Q	380
4381	-	AGCTTAACGGCGAGCGGGACCTCAGAGTGCCAAGGAGGGGTCAAGGAGTGGACCCCCT - 44 L N G E R G P Q S A K E R V K E W T P C	140
4441	<u>-</u>	GCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGCCAGCCCCGGGCAGCCGCCC - 45 G P H Q G Q D E G R G P A P G S G T R Q	500
1	-	AGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGGAACAGGTAAGGATCCCTCTGGGT - 60 V F S M A A M N K E G G T	)
61	-	GGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCCGAAGACAAAGCCAAAGACAGGTGTTT - 12	<u></u> 0
121	-	TTTTCCTTCCCAGCTTCTGTTGCCACCGGGCCAGACTCCCCGTCCCCGTGCCTTTGCCC - 18  A S V A T G P D S P S P V P L P	0
181		CCAGGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCCTTTGGCTGTCCGTAAGTTGGG - 24 P G K P A L P G A D G T P F G C P	0
241	-	GTATTGGAGACATGGGGGTGCTCAGGTGTGTGGTACAGCCAGAGAGACATCCGTGTT - 30	0
301	-	CACTGGTGTCTGTTTTGATGCAGTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGT - 36 P G R K E K P S D P V	0
361		CGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGC - 42 E W T V M D V V E Y F T E A G F P E Q A	0
421		GACAGCTTTCCAAGAGCAGGTGAGTTTCCAGCCCAGGACTACACACAGAGACACAGAG - 48 T A F Q E Q	0
481	-	GGCCTCCCTGGGATGTGCCCTGATCCCGGCTTTCTCTGTTCCTGTCCCACCCA	0
541		GATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCATCCGC - 60 D G K S L L L M Q R T D V L T G L S I R	0
601		CTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTTT - 66 L G P A L K I Y E H H I K V L Q Q G H F	0

FIG. 23C

661 - GAGGATGATGACCCCGATGGCTTCTTAGGCTGAGCGCCCAGCCTCACCCCTGCCCCAGCC - 720
- E D D D P D G F L G \*

721 - CATTCCGGCCCCCATCTCACCCAAGATCCCCCAGAGTCCAGGAGCTGGACGGGGACACCC - 780 781 - TCAGCCCTCATAACAGATTCCAAGGAGAGGGCACCCTCTTGTCCTTATCTTTGCCCCTTG - 840 841 - TGTCTGTCTCACACACATCTGCTCCTCAGCACGTCGGTGTGGGGAGGGGATTGCTCCTTA - 900 961 - ATGTGGGGGGCTTCTCATCTCCCCAAGATCCTCTTCCGTTCAGCCAGATGTTTCCTGTAT - 1020 1081 - ATGCCCCCTTCTCAGTCTGCCCCTGGCCTCCAGCCCCTAGGGGACTAGCTGGGTTGGGG - 1140 1261 - GAAAAAAAGCCACGGAGTCCATTTTATGAATGGGGTGGGGAGAGGGCACTAAAGAGCCT - 1320 1321 - CCTAAGAGAGCCTCAGGTTAGGACAGAATTGTTTGGGGAGGAGAAAAACAGAAACAATG - 1380 1381 - AATTATAGCTGCCTCACAGCCATGTATAACAATAATTGCTCCAGGAAGGTGGGAATATTT - 1440 1441 - GCTTTTTTTTCTTCTGTAATCTCACCGTGTCCGTGTCCAGAACAGAGCTAGGCACACAGC - 1500 1501 - AGGTGCTCAATTTTTGTTTTTCGTTTAGACAGGTTTCATTCTTTCACCCAGGCTGGAGTG - 1560 1561 - CAGTGGTGCTATCATAGCTCATTGTAGCCTCAAACTCCTGGGCTGAAGTGATCCTCCCAC - 1620 1621 - CTCAGCCTCCTGAGTAGCTGGGACTACAGGTGCACTCTGCCATGCCGGGCTAACTTTTAA - 1680 1681 - AAATTTTTGTCCGGGCACAGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG - 1740 1741 - TGGGTGGATCATGAGGTCAGGAGTTCAAGATCAGCCTGGCCAAGATGATGAAACCCTGTC - 1800 1801 - TCTACTAAAAATATAAAAAAATTAGCTGGGCGTGGTGGTGGTGCCTGTAATCCTAGC - 1860 1861 - TATTCAGGAGGCTGAGGCAGAGGATTGCTTACACCTGGGAGGCGGAGGGTGCAGTGAGCC - 1920 1981 - TCTTTGTGTGTGTGGAGATGAGGGTATGCACTTTGTTGGCCAGGTTGGCCTCGAACTC - 2040 2041 - CCAGCCAAGCAATTCTGCCTGGGATTACAAGCGTGAGCCACCATGCCTGGCCTCAAATAT - 2100 2101 - TGTTGAATGGCTAGCAGTTAAGTCCTTGGGTTTATAAGCATTTCCTCAACTGTCCTCCCA - 2160 2161 - AGTCCCCATAAGACAAAAAACTCATAAAATCCCACCTTACAGAAGAGGCAGCTGGCCCGG - 2220 2221 - CACAGAGATGCTGTCTGCCCCGGGTCACACAGGGTGGCATCTGACACCCTGTCTGAGTTC - 2280 2281 - TTCACTCAGAGTCTTTAAATATAATTAGCGTATTTGACATAATGTACATTAAAAACTATA - 2340 2341 - AACCTGTCAGCCTTTGTCTACTGCAAAGAATCCACTACAAATATTGGGGCAGGGATCTGT - 2400 2401 - TCTTGGACCATAGTAGTGTCTCCAGACCTCATGGTCCTCTTCATTAAAACAACAGAAAAT - 2460 2461 - TCCTTCTGGGCCATCAGATGAGACCATGAGATAGAAGATTTCCAAGTGAAGATTTTGTTT - 2520 2521 - CAAGACAGAGTCTTGCTCTGTCACTCAGGCTAGAGTGTACTGGTGCAATCATAACTGTGG - 2580 2581 - TGACAGCCTCGAACTTTTGGGTACAAGTGATTCTCATGCCTCAGACAACACCCAACTAAT - 2640 2641 - ATTTTGGTTTTTGTATAGACAGGGTCTTGCTATGTGGCTTAGGCTGGTCTTGAACTCCTG - 2700 2701 - GCCTCAAGCAGTCCTCCCGCTTCAGCCTCCTAAAGTGTCAGGATTACAGACATGAGCCAC - 2760 2761 - CAAGTCCAGCCTGAAGATTTTTAAAAATTATTGTTAGTAGTAGTCGCCAGAGTTACTACA - 2820 2821 - TCCAAAGTCCCTACTAAGTTCTAAGTAGTCCCTACTAAGTTCTAAGGCAGTTTCTCAACT - 2880 2881 - CATTAGAGTTGTTTTTTGTTTTTAAAGAAAAAAAGGGCTGGGCACTTTAGGAGACCGAC - 2940 2941 - ACGGGAGGATCGCTTGAGTCCAGGAGTTTGAGACCAACCTGGGCAACATGGGCCCCCATC - 3000 3001 - TCTAAAAATTTTAAATTAAAAAAATGTTTTAACAACAAAAAGCGTTCTGGGAGTGAGGGG - 3060 3061 - CTGGGGCCTGGGCGGCTCATTCCATATACCTGTGCCGGGTTGAGGGGTTGGAGACACGT - 3120 3121 - TTAGAGACCCCTCCACTCTAGGAATCCACCTCGAGAGATAAAGGTCCCGGCCCTAGCCAC - 3180 3241 - CTGGAGCGCGTGCGGCGCGTGTGCAGGGGTAGGGGGCCGCAGGCGCGCGGACTGGAGAGG - 3300 3361 - GCTCCGGTGGAGAGGTCAAGGCAGGGCCAGTCGGAGGCTCCCGGGGCGGGGTCGAACCC - 3420 3421 - GCGGCCAACCTGAGCAGCAGCGGAAGCTTAAAGAGCTCAGGTTCCCGCCCCCGGCCCTA - 3480 3481 - CCATGGCTACAGAGCAGTGGTTCGAGGGGTCGCTCCCCCTGGACCCTGGAGAAACACCGC - 3540 3541 - CTCCAGACGCCTTGGAACCTGGGACGCCGCCTGCGGAGACCCCTCCAGGTCGACGCCCC - 3600 3661 - AGGCCCGGGCCTCCACGTCTTCCCCCAAACCTCTGGTCCCCGGCCTGGGCCAGCACCTC - 3720

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				2700
		CCCGCCTATCCCTGGACACTTTGTTCAGCCCCATCACCCAACAGCTGCGCTACCTAC		
3781	-	AGAAGGCAGATGATTTCCAGAGCTACTTGCTCTACAGGTGATGCTGGACAGGGTCCCAGG	-	3840
3841	-	${\tt TCCCCATGGGTAAGGAGACTTGGAGGGGGGGGGGGGGGG$	_	3900
3901	_	GCAAAATTACAAGCGCTAGGAGCCAGAGGGAGACAGTGGAAGAAGCTAGCATATTAGAAT	-	3960
3961	_	CCAGTTTAAGAGAATGAGGAAGACTGTAGAATTGCGGGTAGGGGATGGCTGCTATTACTG	_	4020
		TCGTGGCAGGGTGGGCCTGGGGTTGTCAAGTCTCTAGGACTTTTTCTCCCAGTTTTTAAG		
		TGCTGTCTTACATTTTGAGCCCTGTGCTGGCTAAACAAGACCCACCTGAGCCAAACTTGG		
		CCTGCAGGACATCAGTTTGAGACTCCAAAGGATAATGTGATTCCCAGACCAGGTTTCCCT		
		GTGACTCTCAATTTCAGTGTCCATTGGAATTTCCTAGGAGGCTGGGTTGGGTTTGTTT		
		GTGTTTGTTTTTGAGATGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGTGCAAT		
		CTCAGCTCACTGCAACCTCCGGCTCCCGGATTGAAGCAATTCTCTGCCTCAGCCTCCCGA		
		GTAGCTGGGATTACAGGCGCCCACCAACATGTGTTGCCCGGCTAATTTTTTTT		
		AGTAGAGACAGAGTTTCACCATCTTGGCCAGACTGGTCTTGAGCTCCTGACCTCATGATC		
		CACCCGCCTTGGCCTCCCAAAGTGCTGGAATTACAGACGTGAGCCACCGCGCCTACCCGA		
		GGCTGGGTTTTTTTGTTTTGTTTTGTTTTTTTTTTTTTT		
		$\tt GTCACCTAGGCTGGAGTGCAGTGGGGCGAACTCAGCTCACTGCAACCTCCGCCTCCCAGG$		
		${\tt TTCGAGGGATTCTCATGAGGCTGTTTTTTTTTTTTTTAATGAGACAGGGTCTCGCTCTGTC}$		
		${\tt ACCCAAGCTGGAGTGCAAGTGGGGCAGTCATAGCTCACTGCACCCTCGAACTCCTGGTCT}$		
		${\tt CAAGCAATCTTCCACCTCCCTGGGTAACTGGGACTACAGGTGCCACCATGCCCAGC}$		
4861	-	${\tt TAATTATTTTGTGTAGAGATGGGTTCTTGCTATGTTGCCTAGGCTTGTCTGGAACTCCT}$	-	4920
4921	_	GGCCTCAAGCAATCCTCCAGCCTCAGCCTCCCAAAACTCTAGGATTGCAGGCGTGAGCCA	-	4980
4981	_	CTGTGCCCAGACCCTGCAGGAAGCTCTGGGTCCTAAGTGTTGTGACACTCAGGTGTCAGC	-	5040
5041	_	${\tt ACTTTAACAAGTGTTCCAAATGGGTTTGATGCAGGTAAACCAGAAAGATGTTCAGAAAAG}$	-	5100
5101	_	ACCTGAAACTGGGGGCTTTTCTAATGGGTCAAAGCCAGGGATACAGGTTGGGATTGAGTA	-	5160
5161	_	GAATGGGGAAAACTGCGGGGTGGGGAGGGGTTGTGAGGGATTCCAGGCAAAGGCCCCCTT	-	5220
		CTTCCTTCAGCAGAGACCAAGTACAGAAGGAGCAGCTGGCCAAGGCCATGCCCACCTTCT		
		TACAGATGTGTGAGCCCTACTTCCTGTACCTGGAGGCAGCCGCGAGAAGCATACCCCCCA		
		TCTATGGACCCCTGCAGGAGCTGGTCCGAAAGGGGGTGTGTGGAGGTTTCTTAGACCCCA		
		CGCCCCTTTCTCCGCAGCTCTGAGCCTGTGGGGATGGTGGAGGGGGAGGCCCACTCCT		
		CGCAGGCCAGCTGATCTCACTGTACCCCCCTCTTGTATGCAGCTGTTAGAGATCTCCCAA		
		CAGCTGACCCTGCGCCTGGAACAGCTGGTCCTCATGTACGCTTCCTTTTGGGTTCGTGGAC		
		CTGGAGGAGATGAACCCCCTTAGGTAAAATGGTAGGAGACTCAGATGGGGGGATGAAGGA		
		GTCCAAGGCCCAGCCTCACCCCTCCATTCTCTCATGTCTCGCCAGCATCTCCTGTTTCTT		
		TTGCGGGAGGTTCTCCATCAGCCTGTCCCATGAGGTCTCCATCTTCAGATACTGTGCCCC		
		AACCGCCTACACCGCCTTCCCCCGCTACCTCTATAAGAAGATGCGCTGGCACCT		
		GGAAGCCACCCCAGAGGCCCCTGGTCGGGGACAAGATTCCCTTGTGGATTAGTAAGTCCT		
		CTTACCCAAATCAAAGTCCTCCCCTTTCTATGATGAATGCCAATATGACCCTCCAAACCG		
		TCACCAGCAAAGTGAAAAGTGAGCCAGGGCCCGAGGCAGTGGCTCACGCCTGTAATCCCA		
		ACACTTTGGGAGGCCGAGGCAGGAGGATCACTTGAGCTCAAGAGTTTGAGATCAGCCTGG		
		GCAAGATGGCAAGACCCTGTCTCAACAACAAAGAAATTCGCCAGGCGTGATGGCTGGC		
		$\tt CTGTAGTCCCAGCTACTTGGGAGGGTTAGGCAGGAGGAGCACTTGAGCCCAGGAATCAAG$		
		${\tt GCTACGGTGAGCTGTGATTGTGCCACTGCACTCCACCCTGAGTGGAAGCAATAATCTGTC}$		
		TCTTAAAAAAAAAAAAAAGTGAACCAGGAAACTAAAGGCTTTTGAAAGGCTACCTCTATT		
		TTCTTAAAACCCACCCTCCCACCAAAATAAAAGTTCTCATCTTAAAAGTAGGCTGGCAGG		
6361	_	GAGAAAAGGCCTTGGAGTCACATTCCTACCTGAGAACTTCAGGGCAACTTCTGATGAGTT	-	6420
6421	_	CCCACCTCAACTCCAAAATTAAAGCCCTCAACAGAAGTAGCTAGGAAGCTGATCACTTCT	-	6480
6481	_	AATTACAGCTCCCTCCTAGCTACTTTCTGTGCTATCGAGATACTTGGGAAGACAC	-	6540
6541	_	AGGCCAGAGTCCAGCCAATTCGTGCCCACAGATCCAGAAGCTGTGGTCCATCGGCCGATG	-	6600
		GGTGCCCCTAGGACCAGCCGAGGATGACCTTTATTCATGGTAGGAGCTAGGGCAATAGCA		
		ACGTGGGCCTGGGAGCTGGAGGGGGGGGGCAGAACCCCACCAAAGACAATCCACCTTCCCA		
		AACACTTTGCTTCCCTTAGTAGTGATAGCATTTTATTGTGCCCTGAAAAGCACTTCATGC		
		AGACCCCAGTAACAACCCATGGAGATCTATGCTATTGGCCCCCATTTAACAAAGAAAACAG		
		GGTGCTCAGAGAAGTTGTTACCTGCCCAAGGACACACAGCTAGCAGAGCGAATGGACAGG		
		TCAGGACCAGTTATTCAGCCTCTAGGAGCCATTACTAAGTCTCTGATCAACAAGGAAACA		
		AGTTTCCCCGGGGGTTTTTCCCACCGCAGCTGAAACAAAGCCTCTTTCACCTGAGCCT		
UJUL				

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7021 - CTCACTCAAAGGGAGGGACTCCCGAGGGGGCAGGGGGCACTCAAGTCCAGGCCTGTCTATC - 7080 7081 - CCTGGCCCCCCACCCCAGGATTTTGTGCCCGCACCGCTTGGGGACTACCAGCAGCTGCT - 7140 7141 - GACCATCGGCTTCGAGGAGCCCACGCCCACGCTGGCCACCGACCTGCTGGTGCAGATCCT - 7200 7201 - CACGGGCCAGGCCAGGCCGGCCTCCGAGCGCAGCCGGGCCTGCGGGGTGGGCAGC - 7260 7261 - GCAGGGGTCTTGAACCTGGGGAAGAGGGTAGGAGCTGGAACTTGACAGTTCCAAACTCCA - 7320 7321 - GAATAGGGGGCAGGGGGGCTCACTCGTTCTCGCAGTGCAGCCGGGCCTCGCCTTCCA - 7380 7381 - AAGGGCCAGGCCGAGCTGACCTGTCTGCACCGAGTCCGGCTTGGCCGTGGGGCCCTGAAT - 7440 7441 - GCGGACACGTCAGTTTTGTGTTAAATAAAAGAAAGAAGAGGTCACAGGCTCAGCGTCCG - 7500 7561 - AAATGTAGTCTTTTGAAAGAAGCCTGGAATTCGCCAATAGGCGGACGAGAGTTTGGCGCA - 7620 7621 - TGCGCATAGGCGCACATGAAGCAAAAAGGGAAGTGGTGCCCGTCAACACCGGAACCCAGA - 7680 7681 - AAACTGCAAGTTTAGGGTACCGGGGAAATTCAACGTCCACTGGAGGAAGAGACTTAAGGC - 7740 7801 - CCCGACGCCCCCAGGAAAGTGCCCTCGATCAGTTTCCTAAGGGCCCGAGTTAGACTTTT - 7860 7921 - TCCGGGGTGCGGACAAGGTGGGAGAGCCCTACGGTATCCAAGCTT - 7965

FIG. 23F

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_	
1 -	CAACATGCTTGGGACCAGAAGTGTTTCCAATTTGGGATTTTCTCAAATTTTACCGGTTGA - 60
61 -	GCTTCCCCAATCTGAAAATCTGAAATCCAACATGCACGGCTCTGAAGTCTTTCACTGAGC - 120
121 -	CTTTGGGGGAAATATTTAACATCCTAACAGCCCTAAACCAACGCTCAATTAGCACAACAG - 180
181 -	TTTACAATCTTCTCTACCCACAGCCTGATGCGAGGCTCTGGGACTAGACTATTTAGCCAA - 240
241 -	CAGTTCTTGCAAAATTAACTGACTTATAAGTAAATAGTAATTTCAACACCTCACTGCTAA - 300
	TGCTGTAACAACTCTGCAGACCTAGGGAGCAAGTACGGTTTGCAGAGCACTGGGAAGGCT - 360
	CTGAAGTGACCTTTGAACTGGGCCTCAAAAAATTTTTGGGTTTGGCAAAAGTCAAATCTCT - 420
421 -	TAGGCTTCAAATTCCAGGCACAAGGATTGTTGGGTTTGATTTCATTATCCAGAAGCAATG - 480
	GGGATACAGAATTGTGATCTCATGTGTAGGGAACTGTGGGGGTTTTTTCTACTTTAACCC - 540
541 -	CAGTGAGACTTTGTAGAGTGTGGGGTAGAGAAAAGGCTCATGAATATGCCTGAAGCCTAA - 600
601 -	CTCAGCACCTTTCTGAGGAACTGACTGCCAAAATGGTAATGGAGAGGGGAAAATATGACC - 660
661 -	TACTTTCACAAGTTACCTTGACTGCCTCAGGGAAACCTGCTGTGGTAGTGTTTCTTCTGG - 720
721 -	GTGAAAGACCAGGTAATTACCTGGGTGCTGGTCTCAGACTTACCAGTTTTGAATCCCTGT - 780
781 -	TTTAACCACTCACTATCGATATGACCTTGGATAAGTTACCTAACCTTTCTCTTACTGTCC - 840
841 -	
	GCTATTAGATAGCGGGAAAGCACACAGTAAGCGTTCAAGGAACTGCTATTGTTATTAAAA - 960
	GCCTCCTTTGGAAGAAGGACATTGAGGCCCAGAGAGAGAACAGAACGTCCAGCCACACAG - 1020
	CAAATCCGTGATGAAGTTGGGACTGGAGTATGGGTCTCCTGAGTCTCAGCCCAGGACTCT - 1080
1081 -	ATCCCTCTTCCCGAGTCCTCGGAGTTCCCGGATGGAGTCACATTTGTTCACGGCCAGGGA - 1140
1141 -	GGAAGGTTTGATGGAGGCCTGCAGGAAACAACAGCCAGGCGCAAGGCTTTGGGAGTTGAA - 1200
1201 -	GCATAGCTTCTGCGAGATAGAAACAAGGTTGACATGGGCACTCGTGCAGAATGACGGGCT - 1260
1261 -	CCTTTTGGACTCCCAGGACTACAGTCCCTTATGCACCTTGGGATCTGCGGCTAGCCCCTG - 1320
	CGTAAAGAGGGACGCGTAGTCTTTTCCCTGCCCCGCCCTGCCGGGGCGCCCCGCCTCCGAG - 1380
	GCCGCCTCGCTTCGTCCTTCCCAGCAAGCTCCGCGCCGGCCG
	AGGCGGGAGCAGGCGGCTGGCCGGCAGCAGTTACTCGGGGTTTCCGGTGCGAGGCCAGAG - 1500
1501 -	GTGGGGAAGCCATCGGACGTCGGCGGTGAGGTACGTGCAGCGGCGGCGGCGGTGGGCGAGAC - 1560
1561 <b>-</b>	TATTTGAGAGTGTGCGGGCCGGGATGTTCTCGGCCTGTGGGGAAATCACGCCAACTCCCC - 1620
1621 -	GCGTGGGCCGGGGCTGTCTGGGGATATGCGCATGCGCGGGCGTGCCTCGCGGCTTGAGG - 1680
1681 -	GCGCGCGGGGCGTGGCTGCGCGCGCGGGGGGCGCACGTGGGGCCTGAGGGGCGGGG - 1740
1741 -	GCGGTGCCGGGAGTCCCGCCACGTCAGTCTCCGGCCCTGAGCCAATCCCGCGCCCGGCCT - 1800
1801 -	GCCGCGAGGGGCCGGTTGTGCCGGGAAGTGGCTCCAGGGAAGAGAGCCTCTTCCCTCA - 1860
1861 -	CCCGCTGTGGGAGCTGCGCCCGAAAGCCTGCCCCGGCACGTCGGGCTCTCCTGACCCGC - 1920
	CAAGACCAGAGAGCCGTTGGCGCCCTCCGCCCGGGCCTGCCGGTCCGTTTATTTTAAGAA - 1980
	GCTTTGTGCGCCTGCTGTGGGGATTTCTGATCCAGGCTGCGAAGAATTTCGAAGTCTGGA - 2040
1981 -	GCTTTGTGCGCTGCTGTGGGGATTTCTGATCCAGGCTGCGAAGATTTCGAAGTCTGGA - 2040
	**************************************
2041 -	AAATAGCAACTGTGTTTGTTTCTAAAGGATCTTCTCCTGACCCAGCATCGCTCATCACAA - 2100
-	M
2101 -	TGAAGAACCAAGACAAAAAGAACGGGGCTGCCAAACAATCCAATCCAAAAAGCAGCCCAG - 2160
_	K N O D K K N G A A K O S N P K S S P G
2161 -	GACAACCGGAAGCAGGACCCGAGGGAGCCCAGGAGCGGCCCAGCCAGGCGGC
2101	
-	Q P E A G P E G A Q E R P S Q A A P A V
2221 -	TAGAAGCAGAAGGTCCCGGCAGCCAGCCAGGCTCCTCGGAAGCCGGAGGGTGTGTGCCAGC - 2280
-	EAEGPGSSQAPRKPEG
2281 -	TCTGCGTTGCCAGCGGGCAGGGGGAGGAGCTGTGGGGTCGGCCTCGCTTCTGGACTTACA - 2340
2341 -	GGCCGAGGCCAGGTTGTCCGGGAGGAGGAGATGTAGAATGAGAGGACAGTGCTGGGGGCC - 2400
2401 -	GCGGTCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCCTCTAAGCACAGGAACAGA - 2460
	GTTCTGGAGAGAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGTC - 2520
2401	01101001100110001111111010110001100011000110001100011010

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2581 - 2641 - 2701 - 2761 - 2821 -	- AGGAAATCCAGGTCCCGTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGTT - TGAGGCATTTCTAGAATGATCTGAATGGCAAGAAATGGGTTTTGTGGGGGGGAAGGAGT - GGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTTACATACTTTTATGATCT - AACAAATATGTTCGGGTGGTAGTGAGAAATAGTTGTCTCATAAACAGACTT - AAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTTAAAAGATGTTTCGAATCTAAAT - TCTGACAGGAACTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAAA - AAAAAAGTTAGGCAACATTTAACTCAAACTGATGAGTTTGGCTGGGCCTGAAAAAATCCCA -	2640 2700 2760 2820 2880
2941 - -	- ACCAGTGGTATAATCGTCTTCTTTCTCACTCTACCCCTCATCCTCTCCTGCTGTAGGGGC -ACCAGTGGTATAATCGTCTTCTTTTCTCACTCTACCCCTCATCCTCTCCTGCTGTAGGGGC -ACCAGTGGTAATCGTCTTCTCTCTCTCTCTTCTCACTCTACCCCTCATCCTCTCTCTTAGGGGC -ACCAGTGGTAATCGTCTTCTCTCTTTTCTCACTCTACCCCTCATCCTCTCTCT	3000
3001 -	- TCAAGCCAGAACGGCTCAGTCTGGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGCCGCCA Q A R T A Q S G A L R D V S E E L S R Q	3060
3061 -	- ACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGGCCCCGGCGAGGA - - L E D I L S T Y C V D N N Q G G P G E D	3120
3121 -	- TGGGGCACAGGGTGAGCCGGACCTATGTGGC G A Q G E P A E P E D A E K S R T Y V A	3180
3181 -	- AAGGAATGGGGAGCCTGAACCAACTCCAGTAGTCAATGGAGAGGAAGGA	3240
3241 <b>-</b>	- GGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCATCGAAG - - D P N T E E I R Q S D E V G D R D H R R	3300
3301 -	- GCCACAGGAGAAAAAAGCCAAGGGTTTGGGTGAGCAGAGGGCGGCTCTTTGTGAAGC - - P Q E K K K A K G L G	3360
3481 3541 3661 3721 3781 3841 3901 4021 4081 4261 4321 4321 4341 4561 4561 4621 4681	- AAAGGAAAACGGTACTTCTCAGAGCAGCAAGTCACTCTAGTCTAATCAAAGCCAGGGATG - TGGGGGCCACGGCATAGAGAGAGTGCAGGAGTTACCAGCACAAAGCCTTCTGGGTTTTGGA - GCAACTGGAGCTTGGCATGGGACCTGTTCTCTCTTTTGAGAAAATGAGACGGGAGGCTAG - GGTAGGCTCCTGTGCCAGCCAGTACTACCTGCTGTGTGACCTTGGGTGTCCCTTCTCC - TCTCTGGGTCTTAGTTTATATTTCTCTTTACAGTAAGAAAATTAGACTAGGCCAGAGTTG - AAAACCCAAATATCTGCATAAGCTGGGCCTAGCCATGGGGCCACCTGAAGATGGAGGCTT - TACTGCTTCCCTGATTAGTTGCTCCACTAGCCAACTGAGAGCAGCAAAACTACAGGCT - GGGTGCAGTCAGGCTTTTTTTTTTTTTTTTTTTTTTAAATAAA	3480 3540 3660 3720 3780 3960 4020 4080 4140 4260 4320 4380 4440 4560 4680 4680 4740

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ATHEROSCLEROSIS

4801 - TGACAGGGTGAGACTCCATCTCAAAAAAAGAAAAAGGAAAAAATCTTAACGTCACATACA - 4860 4861 - TGGAAAGATCATCTTTTCACCCCCCACCCCCAACTGAGATGGAGTTTTGCTCTTGTCAC - 4920 4921 - CCAAGCTGGAGTGCACTGGCGCGATCTAGCTCCCTGCAAGCTCCGGCTTCCCGGGTTCACA - 4980 4981 - CCATTCTCCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTGCTACCATGCCC - 5040 5101 - GTTTTGATCTCCTGACCTCGTGATCCGCCCCCCCCCCCAAAGTGCTGGGATTACA - 5160 5221 - TCGCTCTGTCCCAAGCTGGAGTGCAGTGGCGCGATCTGGGCTCACTGCAACCTCCGCCTC - 5280 5281 - CTGGGTTCACGGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTG - 5340 5461 - GCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTAAGCCACTGTACCCTGCCTTTTTTT - 5520 5521 - TTTAATTAATTTATTTTTTAGACAGAGTCTCGCTCTGTCACCAAGCTGGAGTGCAGTGG - 5580 5581 - CGCGATTTGGGCTCACTGCAACCTCCGCTTCTTGGGTTCAAGCGATTTTCCTACCTCAGC - 5640 5701 - GTCTTTAGTAGAGATGGGGTTTCACCATGTTAGGATGGTCTCGATCTCTTGACCTCGTGA - 5760 5761 - TCCGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCTTGCCTGGCC - 5820 5821 - GAAAGTATCTTCATTTTAAAGTTCACTGTTTGGCTACTCTGTTGACAAGAGTTTAGTATT - 5880 5881 - TCTCAAGGAGGCTAAGATACCTATTCCTTTTTGGATCCTACCTCTATCAGGAGGGTGGGC - 5940 5941 - CTTCCTTGCATTGAAACAGTATGAAAACAGTAGCCCTGAATTCATAAGTGGGACACCTTT - 6000 6001 - CTTCTATTGGTAGAGCAGCAGTTTTTTTCTCCTGCCAATGGTGCCTACTAAGGAGATTT - 6060 6061 - CACTAGGGTACAGTCGTTCATTTGATAAGCATTTGTTGAGCATATCCTCTGTGATGGTAC - 6120 6121 - TATGGACAGTACTGGGGCTATAGTGAGGGCAGGATTGAGTTGGTCCTTATGGCAAGGAAG - 6180 6181 - GCAGCTAATCAACAAGCAAAATATAAAGTATGATGGGGAGGGCTGTCTTCAGCACTCATG - 6240 6241 - AGTGTGAGCCCAGGCCTGGAGGGGACACCTGGAGAAGAGGGGTGCATGTCTTTGCTCCTGT - 6300 6301 - GCTTTTCAGGGAAGGAGATCACGTTGCTGATGCAGACATTGAATACTCTGAGTACCCCAG - 6360 K E I T L L M Q T L N T L S T P E 6361 - AGGAGAAGCTGGCTGCTGTGCAAGAAGTATGCTGAACTGGTCAGTTCCCCCCTCCGCG - 6420 EKLAALCKKYAEL 6421 - GGCACCTTCCCTGCGTTGGGAAAATCAGCATGCCACCTGGTGTAAGGTTGGGGGTGCAGA - 6480 6481 - GTCAAGTAGGTGGCTTAATTCCTGTTCAGCTTTTCTCTGAACTATCTGTTAAATGGGGAA - 6540 6541 - TCACTTCCAGCCAGCCTCTTCAGGGCTGTGCAGCAAGAGGAGAAACTGCATATTCCTTGA - 6600 6601 - AAGAAATTTCTCAAAGAATGATTCCAAGGTGGTAGAGCCCTTGTTCCTGGCCTGAGTCCA - 6660 6661 - AGACACCTTGTGATCTTGATGCTTCTTCCTCAAATACAGATGCATAGAGCCATTATCACA - 6720 6721 - GTTAATAAAACTAACACTAGTCACTTGATACTTTTTCCTTTTACTCCAGAGCAGTCTTCT - 6780 6781 - TGTCACTGCCTCCTCATATTCCCCATGACATTGACTTTTAACAGAAACTAGACTAGCTGT - 6840 6841 - CTTGTAGGATGCCCCCTTCTAGCTTTGTCATCTCTGTGGTATCATTTTACTTCTTTACCT - 6900 6901 - CCTGGTACATGTAAGTGAAGTAGAAGTTAGCTCTAAAGCTTGATCCAATTCAGCTTCAAC - 6960 6961 - TTTTTGACAAGAATTCTTCATAAGTACTTCATGTTCCATCACAATAAATGCAAAGCATGC - 7020 7021 - TCTTCCCACTTTGTTAACATTGTTCAGTGGGTTGGGGGTGGGGCAGCCAGATTCTTCC - 7080 7081 - ATCATCAGGTCCCTTGTCAGAATTTGAACTAACAGATTTATCCATTGATGGTCACAGCCT - 7140 7201 - GGGGTCTTGCTCTGCCCCAGGCTGGGGTGCAGTGGCACGATCTCGGCTCGCTGCAAGC - 7260 7261 - TCCGCCTTCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGTCTACAG - 7320 7501 - CAGAGTCAGAGTCTCGCTCTGTCACCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCATT - 7560 7561 - GCAACCTCCACCTCCCAGGTTCAAGCGAGTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGA - 7620 7621 - TTACAGGTGCATGTCACCATGCCTGGCTAAATTTTGTATGTTTTAGTAGAGACAGAGTTT - 7680

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ATHEROSCLEROSIS

7681 - CAGTATGTTGGCCAGGATGGTCTTGATCTCTTGGCCTCGTGATCCGCCCGTCTCAGCCTC - 7740 7801 - AATTAATTCATTCCACACACATTTATTAATATTTTCCTGTAAGGAACTTTACTCATCTTT - 7860 7921 - AGGAAGATAAGCACCCTTTTGGAGTGATCCAGCCAGGGGAAAATTGCTGATGCAAGAGAG - 7980 8041 - GGGGGCTTGGCTGTGAACCACATGGCTAGGTCTGTGTGACTGGAGGAGGACGGGGC - 8100 8101 - AGGTGGACTGGTAGATGTGCAGCTTGTGCCCCTGATTCTCTAGTTTCTTCTGTGTTTTTGA - 8160 8161 - GATTTGATGAGAACGATGAAATAGTTGTCTGGAAGGAGGAGGAGTGTGAATAGCATATGCA - 8220 8221 - TTGTATTGGGATTGCTGGTCTTCCTGAAATTGGTGGCCATGAATTTAAAGTGAGACTCTT - 8280 8281 - CAAGTAGGGTTGTTATAGTACTGGTGTAAAGCAGGAAGGTGCTTTACTAGGGTTGCAGTA - 8340 8341 - CTACTGGGGAAGGGCCAAGAGAGTTGAGGGTGTAAGAAATCCAAGCCAGGTAATGTAGTT - 8400 8401 - ATTTTAAAGGAGAGGAGGATGGTTGAGTCAATGGATTGGAGGTCCTATAGGGTAAGA - 8460 8461 - GACTTTCTGAGGATCACAGATACTGATTGGAATGAGCTAAAAAGATAGGTGATGGTAGTC - 8520 8521 - CTGGACTGGGATGCTGGAAATTGAGATAGTGGGTGTGCTCTCTGGTAGTGACAAATCTAG - 8580 8581 - ATCTGCGCTGTCCAAGATAAATTCGTCTCTAGCTAATTGACATGTGGCCAGTTTGAATTT - 8640 8641 - GAACATGCTATAAATGTAAGATACACATCAGCTTTTGAAGACTTAAGCAAAAACAAAGAA - 8700 8701 - TATAAAACATCTTTTTGTGAGAGAGTGTCTCAGTCACCCAGGCTGGAGTGCAGTGGCGTG - 8760 8761 - ATGTCCTGCTTCCAGGTTCAAACGATTCTCCTGCCTCACAGCCTCCTGGAGTAACTGAGA - 8820 8881 - TTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCTGCCTCAG - 8940 8941 - CCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACTCCCGGCCTCACTTTTTTACAT - 9000 9001 - TGATTCCGTGTTGAAATTGTAATGTTTTGGATATTAGGTTAAATACATATATTACTAAAA - 9060 9061 - TTAATTTCACCTGTTTTTTACTTTTTTAGTGCGGCCAGTAGAATATTTTTTAATTACTTAT - 9120 9121 - GTGGTTTGCATTATATTTCTGTTGTACAGGCCTGGATAGGGTCATGGGAGGGGAACTGAG - 9180 9181 - CTGGGGAAAGGAGTGGGTTTGTGGAAGAGGTGATGGACTGTGAGGCCAGGGAGTTAGAAG - 9240 9241 - GATTATCTGTTGATACTGAAGTGGCCACAAATGAGAAAAGTAATTGTGTTGGGGAGAGCG - 9300 9361 - TAATAGGCACAAGGTACGGTAGCAGGTGGTCTCATCCTCGGGCATGAGTGTCCAGCAAGT - 9420 9421 - TGGGGAAATGCAACAGCTTGAAGTGGCTCTAGTGGCCCAGAGTCAGAGCTGGAATAGGAA - 9480 9481 - TTGGCATCTGCTGTGTGGCCCCTGCTTGCCCTAGTGAGTTACCATTTCTCTGTCCC - 9540 9541 - TACGGTGGAGCCTTTGGGGTTATTGTGAGTTCATGGGAGGAGCGTGTAAGCACCGGCACA - 9600 9601 - GCATCAGCCCATGAGAGTGCTCCTGGCCTGAGAGGGTAAGGGTCAGGGCAGCTCAGGAGA - 9660 9661 - CCCTAGACCTGCATAGTGATCCCCCCACCAGGAAGGCCCCACAAGATGCTCACCTGCCCT - 9720 9721 - CCCTATCCCTGTCCCCAGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTA - 9780 LEEHRNSQKQMKLL 9781 - CAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAGAGCACCTGCGCGGTGAGCACAGCAAG - 9840 -QKKQSQLVQEKDHLRGEHSK 9841 - GCCGTCCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGGCACAACCGC - 9900 -A V L A R S K L E S L C R E L Q R H N R 9901 - TCCCTCAAGGTAGGCCTGGGCCCCTGGAACAGGTGACTCTGGTTTCCTTGACTTCCACT - 9960 - S L K 9961 - TAATGTTTCTTTCATGGGCTTTCCTCTTAAAAAGTAGTGCAGGCTAGGGCCAGGCGCAGT - 10020 10081 - TATACTTAACCCAATATCCAAAACATTACAATTTCAACATGAAATCAGTGTAAAAAAAGCA - 10140 10141 - AGGCTGGGTGTGGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGTGGATGG - 10200 10201 - ATCACTTGAGGCCAGGAGTTTGAGACCAACCTGGTCAACGCAGTGAAACCCCATTCTACT - 10260 10261 - AAAAATACAAAAATTAGCCGAGTGTGCTGGCAAATGCCTATAATCCCAGCTACTCAGGTG - 10320 Matter No.: 10797-004005 Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS

AND THEIR USE IN DIAGNOSING AND TREATING

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10321 - GCTCAGGCATGAGAATTGCTTGCACCTGGGAGGCTGAGGTTGCAGTGAGCCGAGATTGCA - 10380
10441 - GTGCAGGCTTGTGGCATAGAAATACACTTTCTCAATAATGCCTTACGTTAAGAGAGTACT - 10500
10501 - GCTTGTAATCATTTGACATGTATTAGATAAGGTGAAGGATAAAGTACTAAGAGAATCCAT - 10560
10561 - AATGCACTGGCGTTAGTATTTCTCAATGAAATGACAGTCCCCTGGTAAGCGGAGGCCTGG - 10620
10681 - TTCTGCTGCTTCTATGGTGAGGTCAGTCTGTGGTTACACCAAGTTTAAATACAGCCTTTT - 10740
10741 - AACTTTCTTTTTTATATGTAAAATCTTACATGTAGTTTTTAGAATGAAATTATTATACAT - 10800
10801 - GTACCATTTCATATCCTGTGCCTTTTTTTCACTTACATAACATTTTTCCCTATCAGTAT - 10860
10861 - GTGTAGGGCTATCTTCTCATTATATGGATATATTATCAGTGCCCTAGTTAAAGCATTT - 10920
10921 - TGGGGGTTGTTTACAATTTTTCATTATTACATATAGAACTATAGTGAAAATTCTTGTTAT - 10980
10981 - ATTTATCACTGGTCAGTTATATAGAACTTATCTGTAGGATAAGTCATGGAATTGAAATGG - 11040
11041 - CTAGGTCACAGTATATGCAGATTTTTCATTTTAATAGATTTTGCTGGATTGCCTTCCAGT - 11100
11101 - GAGGGGGCAGTGTGCCTTCCCCATCAAAAGTGTTGAGTGCCTAATTCTGCACAACTTTGC - 11160
11161 - AAACCCTGGGTGTTACTAAATTTTAACAGCTTGGTCTCTGGGGGTACAGAGGGGACAAAT - 11220
11221 - GCACATTAATCTGAAATCTGGAAGAATAGGCCTTAGGAGATCCGACTTGCTTCAGAATGG - 11280
11341 - GGGACGGAGTCTTGCTCTGTGGCCCATCGCCCAGGCTGGAGTGCAGTGGCGCGATCATAG - 11400
11401 - CTCACCACACCTCCGCCTCCCAGGTTCAAATGACTCCTCTGCCTCAGCCTCCCAAGCAG - 11460
11461 - CTGGGACCACAGGTGCACACCATCACGCCGGCTAATTTTTGTATTTTAGTAGAAACGGGG - 11520
11521 - TTTCACCATATTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCACCTCAGC - 11580
11581 - CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCTGCCATGTGCCTGCATTTTT - 11640
11641 - CTAGGGGGAGAATCTCACTTGATGTCACCTGATATACAGAGGGGCCCATTGGAACCCGCA - 11700
11761 - GAGACCATCTGTGGACTAGCTGGGGGACCCTTGTGAGGTAGCAGTGGATGATGGCTCTCG - 11820
11821 - GGCTGACTTCTTTGCCCAGGAAGAAGGTGTGCAGCGGGCCCGGGAGGAGGAGGAGAAGCG - 11880
                      EEGVQRAREEEKR
11881 - CAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACA - 11940
     - K E V T S H F Q V T L N D I Q L Q M E Q
- H N E R N S K L R Q E N M E L A E R L K
12001 - GAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGGTAAGGGTATCACGGACAGCAGTCAT - 12060
    - KLIEOYELREE
12061 - GGCCCAGAAATTGTGAGGTTTTGAGTGTGTGTGCTAGGCACTGGGACAGTACCTTTTCAGGC - 12120
12121 - TTCATCCCATTCTCCCTTTTCTTCCTCCTCCTCCTTGGGAGAGAGTAATGTTATTCC - 12180
12181 - TCATAGATAAAAAACAGGTGTGGAGAAGAGACTCACTTACAGCCACAGCCCCAGGTCC - 12240
12241 - ACAGTGCCTTGTCCCAAATGACTGGGCCAGGCATCTTTTGGAATTAGAACTATCCACATT - 12300
12301 - TTAGAATGGAGGTACATGTATGGACTGTGTTTATATAGCACCCTCAGCAGGGCCTTGGG - 12360
12361 - GAAGCCAGACACATTAATGTATTTATGCAGTAGAACTTCCAAATACTCACCTACATTATG - 12420
12421 - GGCTTACAATGATGCAGGTCAAGTCTGGCTGCCAGCTTATGACAATTTCCATTTTCAGAA - 12480
12481 - CTTTGTAGAATTTGGAATTGCAGGGGAGGGGTGTACCTGTGATCAGTGATGGACTCCAGA - 12540
12541 - GACTGTGTCCACTGATTCCTTGCTGCTCCTGCCACTCAAAAGGCAGAATTTATCAGGCTG - 12600
12661 - TGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAA - 12720
12721 - TACAAAAATTAGCCAGGTGTGGTGGTGCACGGCTGTAGTCCCAGCTACTCAGGAGGCTG - 12780
12781 - AGGCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAATGAGCCAAGATTGTGCTAC - 12840
12901 - AGGATGTCACTCCCTTTGTCACTGCGTTGGCTGCCACCCCAGGCACTTGAATCTTTGGAT - 12960
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**ATHEROSCLEROSIS** 12961 - CTTCCCTGCCAGTCACCTGGCTGTTCTGGGCGCGTTCTCATCATGAGAAGGGAGACCTGC - 13020

13021 - AGCCCCTTACAGGGCTGGCAGAGGACCTGCTCTGGATTAGGCCCTTTCCTAGCCCCTGG - 13080 13081 - GGTGTGGCAGTGGGTGAGACCGGGAAGATCTGCCCTCTTAGGTTCATAGGCCAAAGTGAT - 13140 13201 - CATCCTCTGGGAACAAGCTGCTTGTTTGGTTTGAGGGGGAGTTGGTTTGGTTCTTATCCC - 13260 13261 - TCAGCGCTGAGACATAGAGGCTTCCTGGGCCACTACAGTGAGACACGAACTTCAAGAATC - 13320 13321 - TGAATACCCCCGTTTTCTCTCCCCGCCAAGGCAAAAAAGGACTTAGTACTACCTGTGGAG - 13380 13441 - ACAGGCACCCTCATCATACCCAAACTGGACTTACCTGCTAGGCACCTTCCCCTTCCCCATC - 13500 13501 - CAAAAAATGGAGTTATTTCCCTTATTTCAGCAAGTCCAGTTGATTTTACCTTTGAAGT - 13560 13621 - CGCTCCTCTAGTAGGCAGGACAGCCATTCCTTGGGGATGCACATGTCTAGTCTTTGCCTA - 13680 13681 - GATATGGCAAGTCTTTGCCAACTGAGCTAGGCTGTTATGTTCTTAGAGGCATTGTTTTTG - 13740 13741 - CCCATTCTTCCCATTTACAAGAGAATCAGGGACACAGAAGTGAGGGCTTCCAGCCCCATA - 13800 13861 - ATTCCATCCATAAACCATGTGCTTACCAAGGTCTGACTCACTGGGAGAGAAACGACGTGA - 13920 13921 - GGTTGGAAAGCTGACCTTCCAGAGACTTGGGGCCCATGTTGTGTGTACACATGGGAGTC - 13980 13981 - CATCATATCAGATTGAGATGGGGGGCTGGGCCAAAGTGCCCTGGTCTGTGGCTGTGGGGCT - 14040 14041 - ACCCTGAGAAAGGGAGCGCCTGACAAGCCGACTGCTCCCACCATCTTTGTTGCAGCATAT - 14100 14101 - CGACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCA - 14160 - D K V F K H K D L Q Q Q L V D A K L O O 14161 - GGCCCAGGAGATGCTAAAGGAGGCAGAAGAGCGCACCAGCGGGAGAAGGATTTTGTGAG - 14220 - A Q E M L K E A E E R H Q R E K D F 14221 - GCTCAGGCCCCAGGGTTGGGGTGGGGGTGTGGGAGACAGGCTGGGCTCTGGCTCAGC - 14280 14281 - TCATAGCCGGGTTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCTTGAGTACCA - 14340 14341 - GTCTGAGAGCAGGAAGCCTCAGTGGGTCTGGTGCTTGTGGCTAAAAACCAAACATAGCCC - 14400 14401 - CTGGGGGCTTCTGACAGGATCTGGGGTTCTGTCTTGGAAATAGCTCCTGAAAGAGGCAGT - 14460 LLKEAV 14461 - AGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCACCTGAAGCAACAGGT - 14520 - E S Q R M C E L M K Q Q E T H L K Q Q 14521 - GAGAGCATATAACCTGACCTGTGCCTTCAAGTTTCCCTCACTGGGCCCCATCCTGGGGG - 14580 14581 - TAGTGAAATGGGACCCTCATTCTAGGACTGGCTGTCCTGGCTGCTATGACGCCTTGGT - 14640 14641 - TGAGCTTAGGTGGGCTCAGAGGACTTCATTTGTAGCTCAGAAATGTATTGCTTTTGAGGA - 14700 14701 - GGTAGGAACAGAAGATTTGAAAATCAACATAAAGGCAAAATAAAAGTCACCCTAAGTCT - 14760 14761 - CCTACTTTCCAGGCTTAGCATTTTGGATTATATCCTTCCAAATATATAGCTTTGCTTTGT - 14820 14821 - TTTAAGGAAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACGGGTCTGAG - 14880 14881 - TGTGTTGACCAGAGTGCCTCCCAGAGAAACCCAGTCTTATCTGTGGGCTGCTTTCTCCCC - 14940 14941 - ACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGCAG - 15000 LALYTEKFEEFQNTLSKSS

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ATHEROSCLEROSIS

15001	<u>-</u>		GTA V	TTC F	ACC T	ACA T					ATGO M E			TAA	CTG	TGG'	TCC.	AGG	CC?	AGGC?	4 -	15060
15061 15121 15181 15241 15301 15361 15421 15541 15561 15661 15721		CATC GCAG TTTG TGGA TTTG GCGC ACGG GCCT ATTC	TGG TAT TTT GAC CCC GTG GTT GGT TGG CTT	GGT CAG CCC CCA TTC CCT GTT GCA	GTC TGG TTTT CCT CCA ACC ACC ATT	TCA TAI TTI ATI TGC AAA GGI TGI	AGG GTA GGG GCC AAG CTG GTG GGT	GCA TAC GGG CAG GCT GCC GGA GCC	GGG ACT TTT GCT TTC AAT AGG GGA CAC	CTG' CCA( GTT( GGA( TCC' TTT' CTG( TTA' CTC'	TTAG GGTT GTGC FGCC FTCT GTCT FAGC FGAC	GGAA GTTG GTCA GTCA GCGA GCGT GGGA	GGT CCA TTG GGC GCC TTT ACT GAG CTG	TCA GGG. TTG TCC TTT CTT CCA GTG.	CAG AAT TTG ATC TTT GGC CCA GTG ATT	CCT'GGGGTCTA	TTC GCA TTG GCT GCT ATT AAG CTG CAC	CCC GTC TTG CAT GGA TTT TGA GCC CAC	TCT TTTT TGC ATT AGT CCT AGE	TTGAC TTGTC TGAGA TAGAC TAGAC TAGAC TACC AGGGC AGACA		15120 15180 15240 15300 15360 15420 15480 15540 15600 15660 15720 15780
15781	<u>-</u>	TCTG	тст	GTC	ACA	TAA	CCT.	AGA M		CTA/ K	AGAA K	GAT I	CAA K	GAA K	GCT(	GGA( E	GAA K	AGA E	AAC T	CACC	: -	15840
15841		ATGT:			CCC R			AGA S	GCA( S	GCA/ N	ACAA K	.GGC A	CCT( L	GCT' L	TGA( E	GAT( M	GGC! A	rga E	GG <i>P</i> E	GGTG	G -	- 15901
15902 15962 16022 16082 16142 16202 16262 16322 16382 16442 16502		TGTA' TGTC' GTCTC' GGTG' CTTG' AAAG' TGAAC CTCAAC CCAAC	TGT CAA CCA TAA TTT CCT AAA GCC GGA	TCT. GTG. GTG. TGT. TCT. GTG. GTG.	ACC CAA GGA ATG AGA CTT AAG CCC	CAT AGT GTG TGC AGA TTT GAG TCC CTT	CAG TAA' AAG CTG' AAG' TTT' TTC'	TGA TGC' GGA GTT' GAA TGC TGC GGG	CACA TGTT GCAA CTAA CTAA GGAT AAGCA GGCC	AGCT PCT( AAT( ATGT ACGA PTTTT FGGT ATG( CAG(	PAGC CTCC GGAA PAAA ATGG PGCT PATT ACGT CTGC	ATG CCA GAA AGC AGT GGT CCC GGA	AGG' TGGG AGCA AGCA AGTG AGA' ACC'	TAGA GAGG AATA CAGG AACT TGT CCT CCT GAA TGAA T	AGG: STG( STA( STA( FTT: STT: ATG( CAG( CTG(	TGAC STGA STTT AAGC TAGC TTAT SAGC CCTA	GAT' AGC( GCA( CCA( GTA( FAGA AGT(	TTG CCA SAA SAT SAC CGT ATG CAT	CAC GTC AAA TTC CTT TGT AGA GTT GGC	ACAA GTAG AACG ACAG TCAT CAGG ATCT TTCA		15961 16021 16081 16141 16201 16261 16321 16381 16441 16501 16561 16621
16622	<u>-</u>	CTCA	TTT(	CTT'	rcc	CTA		_												AAAA K I		16681
16682		TCCAA Q																				16741
16742		GGGT <i>I</i> V																				16801
16802	- -	GGCC <i>P</i> P	AGA( E	GGG	GCC' P	rgg( G	GGCT A	rca <i>i</i> Q	AGC <i>I</i> A	P	AGC S	TCC	CCCA	AGG( ? /	STC <i>P</i>	CAG	AAG A	GCG(	CCT P	TGCT C Y	-	16861
16862		ACCC <i>P</i> P																				16921
16922		CCAGG R			SAGA	AGC(	CTGC	STGT	TGG	GTC	ATG	CTG	GGAA	AGGG	SAGC	GGC						16981

FIG. 24G

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16982 - CCTGGCCCATAAAAGGCTCCCATGCTGAGCAGCCCATTGCTGAAGCCAGGATGTTCTGAC - 17041
 17042 - CTGGCTGGCATCTGGCACTTGCAATTTTGGATTTTGTGGGTCAGTTTTACGTACATAGGG - 17101
 17102 - CATTTTGCAAGGCCTTGCAAATGCATTTATACCTGTAAGTGTACAGTGGGCTTGCATTGG - 17161
 17162 - GGATGGGGGTGTGTACAGATGAAGTCAGTGGCTTGTCTGTGAGCTGAAGAGTCTTGAGAG - 17221
17222 - GGGCTGTCATCTGTAGCTGCCATCACAGTGAGTTGGCAGAAGTGACTTGAGCATTTCTCT - 17281
17282 - GTCTGATTTGAGGCTCAGACCCCTCCCTGCCCTTCAGAGCTAAGACAAGTAATACACCC - 17341
17402 - CTGCTCTGGAGGCTCCTTTGATTCTCTAGACCTGGAAAAGGTGTCCCTAGGCAGAGCCCT - 17461
17462 - GGCAGGGCGCTCAGAGCTGGGGATTTGCTGCCTGGAACAAGGGACCTGGAGAATGTTTTT - 17521
17522 - GCGTGGGATGATGTGCTGGTCAGGAGCCCCTTGGGCATCGCTTCCCCTGCCCTTTGGTAG - 17581
17582 - TGCCAGGACCAGGCCAATGATGCTTCTCAGTAGCCTTATCATTCACAGGTGCCTCTCTAG - 17641
17642 - CCTGCACAAATGATTGACAAGAGTCACCCAAAGGATTATTTCTGAAGGTGTTTTTTCT - 17701
17762 - TGTATTGAGGACCTTCCAAGGAAGAGGGATGCTGTAGCAGTGGTGCCTGGGTGCCTGGCC - 17821
17822 - TCCAGTGTCCCACCTCCTTCACCACCCCACTTGGCTCCTTTGCCATCTTGATGCTGAGGT - 17881
17942 - TTGCCACAAGCTTACCTGTGGGTTTCAGTCCTGAGAGGCCACCACCAGTTCCCATCAGCA - 18001
18002 - CTGTCTCCATGCAGCAGTTGCTGGGTCCCATGTCCAGCTGCCTCTTTGGCTTCATGGGTT - 18061
18062 - TTTCTGCTTCCTGCCCCCACCCCCACATGTGCAATCCTCAAGATTTGTCCTGATTCTATT - 18121
18122 - TCCTGGCACCTCCCTGCCTGTCCTTGGGGATTCTACTTCTTCCTGTGTGGGAGCCCATAG - 18181
18182 - CTGTTGTCTAACAGGTAAGAAATGAAATTGAACTATTGACTGGGCCCCAGAAATCCATAA - 18241
18242 - AATGGCTGCAGACAGTTGTTTCTGTGTCCTGTTCTACCCCCACTCCAGTACATAACTACT - 18301
18302 - ATGTACTGTGGAGCCATTCTATATGCTGAATGTTCTGCTGTTGCCAAACTTGCCAGGGT - 18361
18362 - ATTAGCCAGTGTTTGTGCCAAGCAGTTTTCTGGGACAACAGAATGACTCAGACCAAGATG - 18421
18422 - GATAGGATGGTTAGGGCTTTGCTTGTTGTTTTTTTTTTGAAGCTAGTTCATTGTCCTG - 18481
18482 - CAGGTCCCTTCATCTTCCATACCTAGCCCACTCTTTTAGCCCTTACCTTAAATCTCTCAG - 18541
18542 - ATAAGTTGGTTCACAAAGAATGTTAAGTACTGAATCATGTGTGACCAGAGACCAGAGATGG - 18601
18602 - CAAATGAATGGCACACCATTTCTCCTTCTCCTGCCCCAGGGCAGGTACCACTGATCTGCA - 18661
18662 - TCAGAGTTGCCTGCTATTCTCTGGTGTATCCTTCACATCTAGGTGCCCTCAAGCAGCTGT - 18721
18722 - GTGAGTGTTGAGATCTCTGCCATCTCTGGCTGAGATACTGCTGTCCTGTGAAGTGTTTCC - 18781
18782 - CATGACCTTTTCTTCCCCTTTGAATCCCTCTGTCTGGAGTAGTCCTTGCCTCTTCCTGC - 18841
18842 - TCCAGTAGGGCCTTTTCCCTACCCCAGCCCCTGTGCCAGGCTAAGCTGGTACAAGAGCTG - 18901
18902 - CCAACCTCACAGAGTGTTTGCTAGGCGAGAGAGGTGCAGGGAAGAGGCAGAGGTATGCAC - 18961
18962 - CTTCCCCCTTGAAGAGAGGGGAAAGGCCTACAGTGGCCCACATAATTGCCTGACTCACAC - 19021
19022 - TTCAGCTACCTCTTAATGCCTGTGGAGGGACTGGAGCTGCTGGATCCCAGTGTGGTGGTG - 19081
19082 - TAGGAGGCCACAGTGAGCAGGTGGCCCCAGCTGGGTTTCCCAGGTCAGGAATGTGGGCCC - 19141
19142 - CAGGCAAGGTGCAGCCTTTGCTCACAGCTCCATCCATGTCTAGACCTTCAGGCCAGTCTG - 19201
19202 - CAGATGAGGTTCCCTACCTTTTTCTTCTCTTCATTGACCAAATCAACCAATCACTACAGC - 19261
19262 - TGCTCTGCTTCTGCTTTCCAAAGTAGCCCAGGTCCTGGGCCAGATGCAGGGGAGGTGCCT - 19321
19382 - TTTTAGGACCAAGATCTGTGTTGGTTTCTTAGATTGCTAGCTTTTCCTCCAGGGGACCAC - 19441
19442 - AGCAGGTGAAGCTCAAGAGCGCATGGCTCTGCTAATAGTAAATTGTTTTCAGGGCCTTGT - 19501
19562 - ATTTGTTGTTTTCCATGAGGTTATCGGACCATGGGCTGAGCTCAGGCACTTTCTGT - 19621
19622 - AGGAGACTGTTATTTCTGTAAAGATGGTTATTTAACCCTTCTCACCCCATCACGGTGGCC - 19681
19682 - CTGAGGGCTGACCCGGAGGCCAGTGGAGCTGCCTGGTGTCCACGGGGGAGGGCCAAGGCC - 19741
19742 - TGCTGAGCTGATTCTCCAGCTGCCCCAGCCTTTCCGCCTTGCACAGCACAGAGGTGG - 19801
19802 - TCACCCCAGGGACAGCCAGGCACCTGCTCCTCTTGCCCTTCCTGGGGGAAGGGAGCTGCC - 19861
19862 - TTCTGTCCCTGTAACTGCTTTCCTTATGGCCCAGCCCGGCCACTCAGACTTGTTTGAAGC - 19921
19922 - TGCACTGGCAGCTTTTTTGTCTCCTTTGGGTATTCACAACAGCCAGGGACTTGATTTTGA - 19981
19982 - TGTATTTTAAACCACATTAAATAAAGAGTCTGTTGCCTTACTTGTTTCTCCTGACCTG - 20041
20042 - TGTATTCCTTTGTTTCTGGATCTGATCCATTCAGCCCCTTCCATCACTGACTTGTTC - 20101
20102 - AGGTCTGCTGCAGAGCGCCCATGGTGGTTCCCTGGTATCTTACATATTCCACAGTGTCTT - 20161
20162 - TGAGCAGTCGCCACAGCCTCAGGATGCTGGCATATTCACTTGAGCTGCCTGAGTGGAGCC - 20221
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20282 - CCCTGACCTGGGGGCTCACAGGCTAGTGAAGGGAAAAGGTACTTTTAGCTATAGACAGGT - 20341
20342 - CAATGGTGCTGAGAGCAGAGGAGGCCCCTGCCCCCTTCAGCAAGGTGAGGGGGTGATA - 20401
20402 - CCTGGAATGGCCTTCTGAACCACAGGGCAGGTAGAAGATGAACGTCATTTAGTGATTAAA - 20461
20582 - GTTTCAATAGGAAATTGATAGGCTCCAGCAGTAAGGCAAAAGGCATGGAGCCAGGCATAG - 20641
20642 - GCCATTTGAGGCCCAGGTTAAGAGGGGTGGACACTCATCACTGCTATTTGGGTCTGAGCT - 20701
20702 - GTGGGTAGGCTCCTATAGCCCTGGCCTGCCCAAGGGAATTCACAGGGGCCTCTAATTGTA - 20761
20762 - TGCATTCCTTAAGGAGAGCACATTCTCTGTTCAGTTTTTACACCCCCCATTTACCCACCT - 20821
20822 - CAAGCATGGGACTCCTATATGGGAGACATGCTGCTGGTGGCCTCACCCAGCACCCTGTTC - 20881
20882 - TCTCTGGGTCCTGGGTTGGTCAGGCACAAAGGATGATATGTGCTGAATGCCCAGGAAATG - 20941
20942 - GCAGAGACAACCCACCTGCCCTTCCCTCCAGGCCTCCACAAATAGATGTGCCCACAATGA - 21001
21002 - CTGTGACAGTCCCAGCAGAGCCTCTGACCCTTCTAGCTGGGTCCTGATACATGTTTTCCA - 21061
21122 - AACTCTTGGAGATTCCAAGCAAGCAGCTCTGAGAATAATGAGGTTTCTGACCCCCAGT - 21181
21182 - GAAGCAGCTGAGGATGGGAACCACAGGGGTGCTCCCTCTGTCAGCAGCATTACCACTGTC - 21241
21242 - TACTCTAGCAGCTCCGGTGGGGAAGGAGGGGATTTCTGTTGTCCCCAGTCTGGGCCCCT - 21301
21302 - GGTTATTGAAAAAGTTCGGAATTACTCTTTACCCTTGTGGAGTGTTCTGAGTGTTGGAAG - 21361
21362 - TACCCAGGAAGAAGCCCTGAGCAGGTGCCCTCAGGAGCAGTGCCCATGGCTCCCCACATC - 21421
21422 - AGCCAAGAGGCCCAACCCCAGGAAGCCACTCCTGCCCGGGGATGGGGAAGGTGGGCTGGG - 21481
21482 - TGGCTGTGCCCTGGGCCAGCTCACTTGAGCCTGCTGAGCCGCCTGGCCAAACA - 21541
21542 - TGAGCCTCTCTCTGTTGTATCAGATGCTGTTCTGGGGACCTGCGCCAGGAGCCTCTGCC - 21601
21662 - AGCCTCCATCAGGTGCTCAGGTTTCCCTGAGGACTGGAGTCAGGTGCCAGGGAATCGCGT - 21721
21782 - ACTCCTGTCACTTCATCTGCGGCAAAATACAGCCCCCACCACTTACCAGAGAAAACTGTC - 21841
21842 - TGGCATTGTAGAGAGAGGGGTTTTGCCCTCAAAAGACTGTTGCTTACTTTCAGTAGAATG - 21901
21962 - TCAATAGGGCACTGGACTCACTCCATTGATGGCTGTCTTTGCTCGAAGTGTCTTCCTGAT - 22021
22082 - ACTCTGTCTCCCCCCCCCCCCCCCCCCCTTTCTGACAAGCCACCACCATTTTGTA - 22141
22142 - AGGAACTGTAGCTTCTCTGAAACTGCCGGGAAAGGGAAAATCTTTTTAAAATAGACAT - 22201
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FIG. 241